

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

SEQUENCE LISTING

<110> INSERM

<120> Infectious pestivirus pseudo-particles containing functional E1 and E2 glycoproteins

<130> BET 03/P0182 PCT

<160> 26

<170> PatentIn version 3.2

<210> 1

<211> 12573

<212> DNA

<213> Bovine viral diarrhea virus

<220>

<221> CDS

<222> (890)..(1195)

<223> C protein

<220>

<221> CDS

<222> (1196)..(1876)

<223> E-rns protein

<220>

<221> CDS

<222> (1877)..(2461)

<223> E1 protein

<220>

<221> CDS

<222> (2462)..(3583)

<223> E2 protein

<220>

<221> CDS

<222> (3584)..(3793)

<223> p7 protein

<400> 1

gtatcacgaga attagaaaag gcactcgtat acgkattggg caattaaaaa taataattag 60

gcttagggaa caaatccctc tcagcgaagg ccgaaaagag gctagccatg cccttagtag 120

gactagcata atgagggggg tagcaacagt ggtgagttcg ttggatgggt taagccctga 180

gtacagggta gtctgcagtg gttcgacgcc ttggaataaa ggtctcgaga tgcacagtgg 240

acgagggcat gccaaaagca catcttaacc tgagcggggg tgcgccaggt aaaagcagtt 300

ttaaacgact gttagaata cagcctgata gggcgctgca gaggccact gtattgctac 360

taaaaatctc tgctgtacat ggcacatgga gttgatcaga aatgaacttt tatacaaaac 420

atacaaacaa aaacccgtcg ggggtggagg accgtgttat gatcaggcag gtgatccctt 480

atttggtgaa aggggagcag tccacccctca atcgacgcta aagctccac acaagagagg	540
ggaacgcgat gttccaacca acttggcatc cttaccaaaa agaggtgact gcaggtcggg	600
taatagcaga ggacctgtga ggggatcta cctgaagcca gggccactat tttaccagga	660
ctataaaggc cccgtctatc acagggcccc gctggagctc tttgaggagg gatccatgtg	720
tgaaacgact aaacggatag ggagagtaac tggaagtac ggaagctgt accacattta	780
tgtgtgtata gatggatgta taataataaa aagtgccacg agaagttacc aaaggtgtt	840
caggtggguc cataataggc ttgactgcc tctatgggtc acaacttgc tca gac acg	898
Ser Asp Thr 1	
aaa gaa gag gga gca aca aaa aag aaa aca cag aaa ccc gac aga cta	946
Lys Glu Glu Gly Ala Thr Lys Lys Lys Thr Gln Lys Pro Asp Arg Leu	
5 10 15	
gaa agg ggg aaa atg aaa ata gtg ccc aaa gaa tct gaa aaa gac agc	994
Glu Arg Gly Lys Met Lys Ile Val Pro Lys Glu Ser Glu Lys Asp Ser	
20 25 30 35	
aaa act aaa cct ccg gat gct aca ata gtg gtg gaa gga gtc aaa tac	1042
Lys Thr Lys Pro Pro Asp Ala Thr Ile Val Val Glu Gly Val Lys Tyr	
40 45 50	
cag gtg agg aag aag gga aaa acc aag agt aaa aac act cag gac ggc	1090
Gln Val Arg Lys Lys Gly Lys Thr Lys Ser Lys Asn Thr Gln Asp Gly	
55 60 65	
ttg tac cat aac aaa aac aaa cct cag gaa tca cgc aag aaa ctg gaa	1138
Leu Tyr His Asn Lys Asn Lys Pro Gln Glu Ser Arg Lys Lys Leu Glu	
70 75 80	
aaa gca ttg ttg gcg tgg gca ata ata gct ata gtt ttg ttt caa gtt	1186
Lys Ala Leu Leu Ala Trp Ala Ile Ile Ala Ile Val Leu Phe Gln Val	
85 90 95	
aca atg gga gaa aac ata aca cag tgg aac cta caa gat aat ggg acg	1234
Thr Met Gly Glu Asn Ile Thr Gln Trp Asn Leu Gln Asp Asn Gly Thr	
100 105 110 115	
gaa ggg ata caa cgg gca atg ttc caa agg ggt gtg aat aga agt tta	1282
Glu Gly Ile Gln Arg Ala Met Phe Gln Arg Gly Val Asn Arg Ser Leu	
120 125 130	
cat gga atc tgg cca gag aaa atc tgt act ggc gtc cct tcc cat cta	1330
His Gly Ile Trp Pro Glu Lys Ile Cys Thr Gly Val Pro Ser His Leu	
135 140 145	
gcc acc gat ata gaa cta aaa aca att cat ggt atg atg gat gca agt	1378
Ala Thr Asp Ile Glu Leu Lys Thr Ile His Gly Met Met Asp Ala Ser	
150 155 160	
gag aag acc aac tac acg tgt tgc aga ctt caa cgc cat gag tgg aac	1426
Glu Lys Thr Asn Tyr Thr Cys Cys Arg Leu Gln Arg His Glu Trp Asn	
165 170 175	
aag cat ggt tgg tgc aac tgg tac aat att gaa ccc tgg att cta gtc	1474

Lys	His	Gly	Trp	Cys	Asn	Trp	Tyr	Asn	Ile	Glu	Pro	Trp	Ile	Leu	Val	
180					185					190					195	
atg aat aga acc caa gcc aat ctc act gag gga caa cca cca agg gag	1522															
Met Asn Arg Thr Gln Ala Asn Leu Thr Glu Gly Gln Pro Pro Arg Glu																
	200								205					210		
tgc gca gtc act tgt agg tat gat agg gct agt gac tta aac gtg gta	1570															
Cys Ala Val Thr Cys Arg Tyr Asp Arg Ala Ser Asp Leu Asn Val Val																
	215							220					225			
aca caa gct aga gat agc ccc aca ccc tta aca ggt tgc aag aac gga	1618															
Thr Gln Ala Arg Asp Ser Pro Thr Pro Leu Thr Gly Cys Lys Lys Gly																
	230						235					240				
aag aac ttc tcc ttt gca ggc ata ttg atg cgg ggc ccc tgc aac ttt	1666															
Lys Asn Phe Ser Phe Ala Gly Ile Leu Met Arg Gly Pro Cys Asn Phe																
	245					250				255						
gaa ata gct gca agt gat gta tta ttc aaa gaa cat gaa cgc att agt	1714															
Glu Ile Ala Ala Ser Asp Val Leu Phe Lys Glu His Glu Arg Ile Ser																
260					265					270					275	
atg ttc cag gat acc act ctt tac ctt gtt gac ggg ttg acc aac tcc	1762															
Met Phe Gln Asp Thr Thr Leu Tyr Leu Val Asp Gly Leu Thr Asn Ser																
	280							285						290		
tta gaa ggt gcc aga caa gga acc gct aaa ctg aca acc tgg tta ggc	1810															
Leu Glu Gly Ala Arg Gln Gly Thr Ala Lys Leu Thr Thr Trp Leu Gly																
	295						300						305			
aag cag ctc ggg ata cta gga aaa aag ttg gaa aac aag agt aag acg	1858															
Lys Gln Leu Gly Ile Leu Gly Lys Lys Leu Glu Asn Lys Ser Lys Thr																
	310					315						320				
tgg ttt gga gca tac gct gct tcc cct tac tgt gat gtc gat cgc aaa	1906															
Trp Phe Gly Ala Tyr Ala Ser Pro Tyr Cys Asp Val Asp Arg Lys																
	325					330				335						
att ggc tac ata tgg tat aca aaa aat tgc acc cct gcc tgc tta ccc	1954															
Ile Gly Tyr Ile Trp Tyr Thr Lys Asn Cys Thr Pro Ala Cys Leu Pro																
340					345					350					355	
aag aac aca aaa att gtc gcc cct ggg aaa ttt ggc acc aat gca gag	2002															
Lys Asn Thr Lys Ile Val Gly Pro Gly Lys Phe Gly Thr Asn Ala Glu																
	360							365						370		
gac ggc aag ata tta cat gag atg ggg ggt cac ttg tgc gag gta cta	2050															
Asp Gly Lys Ile Leu His Glu Met Gly Gly His Leu Ser Glu Val Leu																
	375						380						385			
cta ctt tct tta gtg gtg ctg tcc gac ttc gca ccg qea aca gct agt	2098															
Leu Leu Ser Leu Val Val Leu Ser Asp Phe Ala Pro Glu Thr Ala Ser																
	390						395						400			
gta atg tac cta atc cta cat ttt tcc atc cca cea agt cag gta gat	2146															
Val Met Tyr Leu Ile Leu His Phe Ser Ile Pro Gln Ser His Val Asp																
	405				410						415					
gta atg gat tgt gat aag acc cag ttg aac ctc aca gtg gag ctg aca	2194															
Val Met Asp Cys Asp Lys Thr Gln Leu Asn Leu Thr Val Glu Leu Thr																

4

420	425	430	435	
aca gct gaa gta ata cca ggg tgc gtc tgg aat cta ggc aaa tat gta				2242
Thr Ala Glu Val Ile Pro Gly Ser Val Trp Asn Leu Gly Lys Tyr Val				
440		445	450	
tgt ata aga cca aat tgg tgg cct tat gag aca act gta gtg ttg gca				2290
Cys Ile Arg Pro Asn Trp Trp Pro Tyr Glu Thr Thr Val Val Leu Ala				
455		460	465	
ttt gaa gag gtg agc cag gtg gtg aag tta gtg ttg agg gca ctc aga				2338
Phe Glu Glu Val Ser Gln Val Val Lys Leu Val Leu Arg Ala Leu Arg				
470		475	480	
gat tta aca cgc att tgg aac gct gca aca act act gct ttt tta gta				2386
Asp Leu Thr Arg Ile Trp Asn Ala Ala Thr Thr Thr Ala Phe Leu Val				
485		490	495	
tgc ctt gtt aag ata gtc agg ggc cag atg gta cag ggc att ctg tgg				2434
Cys Leu Val Lys Ile Val Arg Gly Gln Met Val Gln Gly Ile Leu Trp				
500		505	510	515
cta cta ttg ata aca ggg gta caa ggg cac ttg gat tgc aaa cct gaa				2482
Leu Leu Leu Ile Thr Gly Val Gln Gly His Leu Asp Cys Lys Pro Glu				
520		525	530	
ttc tgc tat gcc ata gca aag gac gaa aga att ggt caa ctg ggg gct				2530
Phe Ser Tyr Ala Ile Ala Lys Asp Glu Arg Ile Gly Gln Leu Gly Ala				
535		540	545	
gaa ggc ctt acc acc act tgg aag gaa tac tca cct gga atg aag ctg				2578
Glu Gly Leu Thr Thr Thr Trp Lys Glu Tyr Ser Pro Gly Met Lys Leu				
550		555	560	
gaa gac aca atg gtc att gct tgg tgc gaa gat ggg aag tta atg tac				2626
Glu Asp Thr Met Val Ile Ala Trp Cys Glu Asp Gly Lys Leu Met Tyr				
565		570	575	
ctc caa aga tgc acg aga gaa acc aga tat ctc gca atc ttg cat aca				2674
Leu Gln Arg Cys Thr Arg Glu Thr Arg Tyr Leu Ala Ile Leu His Thr				
580		585	590	595
aga gcc ttg ccg acc agt gtg gta ttc aaa aaa ctc ttt gat ggg cga				2722
Arg Ala Leu Pro Thr Ser Val Val Phe Lys Lys Leu Phe Asp Gly Arg				
600		605	610	
aag caa gag gat gta gtc gaa atg aac gac aac ttt gaa ttt gga ctc				2770
Lys Gln Glu Asp Val Val Glu Met Asn Asp Asn Phe Glu Phe Gly Leu				
615		620	625	
tgc cca tgt gat gcc aaa ccc ata gta aga ggg aag ttc aat aca acg				2818
Cys Pro Cys Asp Ala Lys Pro Ile Val Arg Gly Lys Phe Asn Thr Thr				
630		635	640	
ctg ctg aac gga ccg gcc ttc cag atg gta tgc ccc ata gga tgg aca				2866
Leu Leu Asn Gly Pro Ala Phe Gln Met Val Cys Pro Ile Gly Trp Thr				
645		650	655	
ggg act gta agc tgt acg tca ttc aat atg gac acc tta gcc aca act				2914
Gly Thr Val Ser Cys Thr Ser Phe Asn Met Asp Thr Leu Ala Thr Thr				
660		665	670	675

gtg gta cgg aca tat aga agg tct aaa cca ttc cct cat agg caa ggc Val Val Arg Thr Tyr Arg Arg Ser Lys Pro Phe Pro His Arg Gln Gly 630 685 690	2962
tgt atc acc caa aag aat ctg ggg gag gat ctc cat aac tgc atc ctt Cys Ile Thr Gln Lys Asn Leu Gly Glu Asp Leu His Asn Cys Ile Leu 695 700 705	3010
gga gga aat tgg act tgt gtg cct gga gac caa cta cta tac aaa ggg Gly Gly Asn Trp Thr Cys Val Pro Gly Asp Gln Leu Leu Tyr Lys Gly 710 715 720	3056
ggc tct att gaa tct tgc aag tgg tgt ggc tat caa ttt aaa gag agt Gly Ser Ile Glu Ser Cys Lys Trp Cys Gly Tyr Gln Phe Lys Glu Ser 725 730 735	3106
gag gga cta cca cac tac ccc att ggc aag tgt aaa ttg gag aac gag Glu Gly Leu Pro His Tyr Pro Ile Gly Lys Cys Lys Leu Glu Asn Glu 740 745 750 755	3154
act ggt tac agg cta gta gac agt acc tct tgc aat aga gaa ggt gtg Thr Gly Tyr Arg Leu Val Asp Ser Thr Ser Cys Asn Arg Glu Gly Val 760 765 770	3202
gcc ata gta cca caa ggg aca tta aag tgc aag ata gga aaa aca act Ala Ile Val Pro Gln Gly Thr Leu Lys Cys Lys Ile Gly Lys Thr Thr 775 780 785	3250
gta cag gtc ata gct atg gat acc aaa ctc gga cct atg cct tgc aga Val Gln Val Ile Ala Met Asp Thr Lys Leu Gly Pro Met Pro Cys Arg 790 795 800	3298
cca tat gaa atc ata tca agt gag ggg cct gta gaa aag aca ggc tgt Pro Tyr Glu Ile Ile Ser Ser Glu Gly Pro Val Glu Lys Thr Ala Cys 805 810 815	3346
act ttc aac tac act aag aca tta aaa aat aag tat ttt gag ccc aga Thr Phe Asn Tyr Thr Lys Thr Leu Lys Asn Lys Tyr Phe Glu Pro Arg 820 825 830 835	3394
gac agc tac ttt cag caa tac atg cta aaa gga gag tat caa tac tgg Asp Ser Tyr Phe Gln Gln Tyr Met Leu Lys Gly Glu Tyr Gln Tyr Trp 840 845 850	3442
ttt gac ctg gag gtg act gac cat cac cgg gat tac ttc gct gag tcc Phe Asp Leu Glu Val Thr Asp His His Arg Asp Tyr Phe Ala Glu Ser 855 860 865	3490
ata tta gtg gtg gta gta gcc ctc ttg ggt ggc aga tat gta ctt tgg Ile Leu Val Val Val Val Ala Leu Leu Gly Gly Arg Tyr Val Leu Trp 870 875 880	3538
tta ctg gtt aca tac atg gtc tta tca gaa cag aag gcc tta ggg att Leu Leu Val Thr Tyr Met Val Leu Ser Glu Gln Lys Ala Leu Gly Ile 885 890 895	3586
cag tat gga tca ggg gaa ctg gtg atg atg ggc aac ttg cta acc cat Gln Tyr Gly Ser Gly Glu Val Val Met Met Gly Asn Leu Leu Thr His 900 905 910 915	3634

aac aat att gaa gtg gtg aca tac ttc ttg ctg ctg tac cta ctg ctg 3682
 Asn Asn Ile Glu Val Val Thr Tyr Phe Leu Leu Leu Tyr Leu Leu Leu
 920 925 930

agg gag gag agc gta aag aag tgg gtc tta ctc tta tac cac atc tta 3730
 Arg Glu Glu Ser Val Lys Lys Trp Val Leu Leu Leu Tyr His Ile Leu
 935 940 945

gtg gta cac cca atc aaa tct gta att gtg atc cta ctg atg att ggg 3778
 Val Val His Pro Ile Lys Ser Val Ile Val Ile Leu Leu Met Ile Gly
 950 955 960

gat gtg gta aag gcc gattcagggg gcccaagagta ctgggggaaa atgacctct 3833
 Asp Val Val Lys Ala
 965

gttttacaac agtagtacta atcgatcatag gttaaatcat agctaggcgt gacccaacta 3893

tagtgccact ggtacaata atggcagcac tgagggtcac tgaactgacc caccagcctg 3953

gagttgacat cctgtggcg gtcagtacta taacctact gatggttagc tatgtgacag 4013

attatttttag atataaaaaa tggttacagt gcattctcag cctgggtatct gccgtgttct 4073

tgataagaag cctaataaac ctaggtagaa tcyagatgcc agaggtaact atcccaact 4133

ggagaccact aactttaata ctattatatt tgatctcaac aacaattgta acgaggtgga 4193

aggttgacgt ggctggccta ttgttgcaat gtgtgcctat cttattgctg gtcacaacct 4253

tgtgggocga cttcttaacc ctaatacga tcttgccctac ctatgaattg gttaaattat 4313

actatctgaa aactgttagg actgatacag aaagaagttg gctagggggg atagactata 4373

caagagttga ctccatctac gacgttgatg agagtggaga gggcgtatat ctttttccat 4433

caaggcagaa agcacagggg aatttttcta tactcttgcc ctttatcaaa gcaacactga 4493

taagttgcgt cagcagtaaa tggcagctaa tatacatgag ttacttaact ttggacttta 4553

tgtactacat gcacaggaaa gttatagaag agatctcagg aggtaccac ataatatcca 4613

ggtagtggc agcactcata gagctgaact gctccatgga agaagaggag agcaaaggct 4673

taaagaagtt ttatctattg tctggaagggt tgagaaacct aataataaaa cataaggtaa 4733

ggaatgagac cgtgcttct tggtagggg aggaggaagt ctccgtatg ccaaagatca 4793

tgactataat caaggccagt aactgagta agagcaggca ctgcataata tgcaactgat 4853

gtgagggccg agagtggaaa ggtggcacct gcccaaatg tggacgcat gggagggcga 4913

taacgtgtgg gatctcgta gcagttttg aagaaagaca ctataaaga atctttataa 4973

gggagggcaa ctttgagggt atgtgcagcc gatgccaggg aaagcatagg aggtttgaaa 5033

tggaccggga acctaaaggt gccagatact gtgctgagtg taataggctg catcctgctg 5093

aggaaggtga cttttgggca gaggcagca tgttgggctt caaatcacc tactttgccc 5153

tgatggatgg aaaggtgtat gatctcacag agtgggctgg atgccagcgt gtgggaatct 5213

ccccagatac ccacagagtc ccttgcacaca tctcatttgg ttcacggatg cctttcaggc 5273
aggaatacaa tggctttgta caataataccg ctagggggca actatttctg agaaacttgc 5333
ccgtactggc aactaaagta aaaatgctca tggtaggcaa ccttggagaa gaaattggta 5393
atctygaaca tcttgggtgg atcctaaggg ggctgcctg gtgtaagaag atcacagagc 5453
acgaaaaatg ccacattaat atactggata aactaacgc attttccggg atcatgccaa 5513
gggggactac acccagagcc cgggtgaggt tccctacgag ctactaaaa gtgaggaggg 5573
gtctggagac tgcctgggct tccacacacc aaggcgggat aagttcagtc gacctgtaa 5633
ccgccggaag agatctactg gtctctgaca gcctgggagc aactagagtg gtttgccaaa 5693
gcaanaacag gttgaccgat gagacagagt atggcgtcaa gactgactca ggtgcccag 5753
acgggtgccag atgttatgtg ttaaattccag aggccgttaa catatcagga tccaaagggy 5813
cagtcgttca cctccaaaag acaggtggag aattcacgtg tgcacccga tcaggcacac 5873
cggctttctt cgacctaaaa aacttgaaag gatggtcagg cttgcctata tttgaagcct 5933
ccagcgggag ggtggttggc agagtcaaag tagggaagaa tgaagagtct aaacctacaa 5993
aaataatgag tggaaatccag accgtctcaa aaaacagagc agacctgacc gagatggtca 6053
agaagataac cagcatgaac aggggagact tcaagcagat tactttggca acaggggcag 6113
gcaaaaccac agaactccca aaagcagtta tagaggagat aggaagacac aagagagtat 6173
tagttcttat accattaagg gcagcggcag agtcagtcta ccagtatatg agattgaaac 6233
acccaagcat ctcttttaac ctaaggatag gggacatgaa agagggggac atggcaaccg 6293
ggataacctt tgcacatac ggttacttct gccaaatgcc tcaaccaag ctccagagctg 6353
ctatggtaga atactcatac atattcttag atgaatacca ttgtccact cctgaacaac 6413
tggcaattat cgggaagatc cacagatttt cagagagtat aagggttgc gccatgactg 6473
ccacgccagc aggtcgggtg accacaacag gtcaaaagca cccaatagag gaattcatag 6533
cccccgaggt aatgaaaggg gaggatcttg gtatgcagt ccttgatata gcagggttaa 6593
aaataccagt gtagtagatg aaaggcaata tgttggtttt tgtaccaacg agaaacatgg 6653
cagtagaggt agcaagaag ctaaaagcta agggctataa ctctggatac tattacagtg 6713
gagaggatcc agccaatctg agagtgtga catcacaatc cccctatgta atcgtggcta 6773
caaatgctat tgaatcagga gtgacactac cagatttggg caggggtata gacacggggt 6833
tgaatgtga aaagagggtg aggtatcat caaagatacc ctctatgta acaggcotta 6893
agaagatggc cgtgactgtg ggtcagcagg cgcagcgtag gggcagagta ggtagagtga 6953
aacccgggag gtattatagg agccaggaa cagcaacagg gtcaaaagac taccactatg 7013

acctcttgca ggcacaaaga tacgggattg aggatggaa caacgtgacg aaatccttta 7073
gggagatgaa ttacgattgg agcctatacg agggaggacag cctactaata acccagctgg 7133
aaatactaaa taatctactc atctcagaag acttgccagc cgctgttaag aacataatgg 7193
ccaggactga tcaccagag ccaatccaac ttgcatacaa cagctatgaa gtccaggctc 7253
cggctctatt cccaaaaata aggaatggag aagtcacaga cacctacgaa aattactcgt 7313
ttctaaatgc cagaaagtta ggggaggatg tgcccggtga talctacgt actgaagatg 7373
aggatctggc agttgacctc ttagggttag actggcctga tcttgggaa cagcaggtag 7433
tgagactgg taaagcactg aagcaagtga cggggtgtc ctgggtgaa aatgcctac 7493
tagtggcttt atttgggtat gtgggttacc aggtctctc aaagaggcat gtccaatga 7553
taacagacat atataccalc gaggaccaga gactagaaga caccaccac ctccagtatg 7613
caccacacgc cataaaaaac gatgggacag agactgaact gaaagaactg gcgtcgggtg 7673
acgtggaaaa aatcatggga gccatttcag attatgcagc tgggggactg gagtttgta 7733
aatcccaagc agaaaagata aaaacagctc ctttgttta agaaaacgca gaagcgcga 7793
aegggatatgt ccaaaaattc attgactcat taattgaaa taaagaagaa ataatcagat 7853
atggtttggt gggaacacac acagcactat acaaaagcat agctgcaaga ctggggcatg 7913
aaacagcgtt tgccacacta gtgttaaaat ggctagcttt tggaggggaa tcagtgtcag 7973
accacgtcaa gcaggcggca gttgatttag tggctatta tgtgatgaat aagccttct 8033
tccaggtga ctccagaca cagcaagag ggaggcgatt cgtcgcaagc ctgttcatct 8093
ccqactggc aacctacaca taccaaaact ggaattacca caatctctct aaagtgggtg 8153
aaccagcctt gggttacctc cctatgcta ccagcgcat aaaaatgtc accccaacgc 8213
ggctggagag cgtggtgata ctgagacca ccatataaa aacatactc tctataagga 8273
aggggaagag tgatggattg ctgggtacgg ggataagtyc agccatggaa atctgtcac 8333
aaaacccagt atcggtaggt atatctgtga tgttgggggt aggggcaatc gctgcgcaca 8393
acgtattga gtccagtga cagaaaagga cctacttat gaaggtgtt gtawagaact 8453
tcttgatca gctgcaca gatgagctgg taaaagaaa cccagaaaa atlatatgg 8513
ccttatttga agcagtcag acaattggta acccctgag actaatatc cacctgtatg 8573
gggtttacta caaaggttg gggccaagg aactatctga gaggacagca gccagaaact 8633
tatccactt gataatgtt gaagccttc agttattagg gatggactca caagggaat 8693
taaggaaact gtccggaat tacattttg atttgatata cggcctacac aagcaantca 8753
acagaggggt gaacaaaaty gtactgggtt gggccctgc accctttagt tgtgactgga 8813
ccctagtga cgagaggatc agattgcaa cagacaactc ttgagggtg gaaaccaggt 8873

gcccattgtgg ctatgagatg aaagctttca aaaatgtagg tggcaaactt accaaagtgg 8933
aggagagcgg gccctttccta tgtagaaaca gacctggtag gggaccagtc aactacagag 8993
tcaccaagta ttacgatgac aacctcagag agataaaaacc agtagcaaag ttggaaggac 9053
aggtagagca ctactacaaa ggggtcacag caaaaattga ctacagtaaa ggaaaaatgc 9113
tcttgccac tgacaagtgg gaggtggaac atggtgtcat aaccaggtta gctaagagat 9173
atacgggggt cgggttcaat ggtgcatact taggtgacga gcccaatcac cgtgctctag 9233
tgagagagga ctgtgcaact ataaccaaaa acacagtaca gtttctaaaa atgaagaagg 9293
ggtgtgcgtt cacctatgac ctgacctct ccaatctgac caggctcctc gaactagtac 9353
acaggaacaa tcttgaagag aaggaaatc ccaccgctac ggtcaccaca tggctagctt 9413
acaccttcgt gaatgaagac gtagggacta taaaaccagt acteggagag agagtaatcc 9473
ccgaccctgt agttgatatc aatttccaac cagaggtgca agtggacacg tcagagggtg 9533
ggatcacaat aattggaagg gaaaccctga tgacaacggg agtgacacct gtcttgaaa 9593
aagtagagcc tgacgccagc gacaaccaa actcggtgaa gatcgggtt gatgagggt 9653
attaccagg gccctggaata cagacacata cactaacaga agaaatacac aacagggatg 9713
cgaggccctt catcatgac ctgggctcaa ggaattccat atcaaatagg gcaaagactg 9773
ctagaaatat aatctgtac acaggaaatg accccaggga aatacagagac ttgatggctg 9833
caggcgcat gttagtagta gcactgagg atgtcgacct tgagctgctt gaaatggtcg 9893
atttcaagg gactttttta gatagggagg ccttgagggc tctaagtctc gggcaacct 9953
aactgaagca ggttaccag gaagctgtt ggaatttcat agaacagaaa aagatgttg 10013
agatccctaa ctggtttgca tcagatgacc cagtattctt ggaagtggcc ttaaaaaatg 10073
ataagtacta cttagtagga gatgttgag agctaaaaga tcaagctaaa gcacttggg 10133
ccacggatca gacaagaatt ataaaggagg taggtcaag gacgtatgac atgaagctat 10193
ctagctggtt cctcaaggca tcaaacaaac agatgagttt aactccactg tttgaggat 10253
tgttgctacg gtgcccacct gcaactaaga gcaataagg gcaatggca tcagcttacc 10313
aattggcaca gggtaactcg gagccctcg gttcggggt gcacctaggt acaataccag 10373
ccagaagggt gaagatacac ccatatgaag cttaacctgaa gttgaaagat ttcatagaag 10433
aagaagagaa gaaacctagg gttcaggata cagtaataag agagcacaac aatgggatac 10493
tcaaaaaaat aagggtttcaa ggaaacctca acaccaagaa aatgctcaac ccagggaac 10553
tatctgaaca gttggacagg gagggggcga agaggacat ctacaaccac cagattggta 10613
ctataatgtc aagtgcaggc ataaggctcg agaaattgcc aatagtgagg gcccaaaccc 10673

acacccaaaac ctttcatgag gcaateagag ataagataga caagagtga aaccggcaaa 10733
atccagaatt gcacaacaaa ttgttgaga tttccacac gatagccca cccaccctga 10793
aacacaccta cggtagggtg acgtgggagc aacttgaggc gggggtaaat agaaaggggg 10853
cagcaggctt cctggagaag aagaacatcg gagaagtatt ggattcagaa aagcacctgg 10913
tagaacaatt ggtcagggat ctgaaggccg ggagaaagat aaaatattat gaaactgcaa 10973
taccaaaaaa tgagaagaga gatgtcagtg atgactggca ggcaggggac ctggtggttg 11033
agaagaggcc aagagttatc caataccctg aagccaagc aaggctagcc atcactaagg 11093
tcattgataa ctgggtgaaa cagcagcccg ttgtgattcc aggatatgaa ggaaagacc 11153
ccttgttcaa catctttgat aaagtgagaa aggaatggg ctcttcaat gagccagtgg 11213
ccgtaagttt tgacacccaa gcttgggaca ctcaagtgc tagtaaggat ctgcaactta 11273
ttggagaaat ccagaaatat tactataaga aggagtggca caagtgcatt gacaccatca 11333
ccgaccacat gacagaagta ccagttataa cagcagatgg tgaagtata ataagaaatg 11393
ggcagagagg gagcgccag ccagacacaa gtgttgcaa cagcatgtta aatgtcctga 11453
caatgatgta cggcttctgc gaaagcacag gggtagcgt caagagttc aacagggtgg 11513
caaggatcca cgtctgtggg gatgatggct tcttaataac tgaaaaaggg ttagggtga 11573
aatttgctaa caaagggatg cagattcttc atgaagcagg caaacctcag aagataacgg 11633
aaggggaaaa gatgaaagt gcctatagat ttgaggatat agagtctgt tctcatacc 11693
cagtcctgt taggtgtcc gacaacacca gtatgcacat ggccgggaga gacaccgtg 11753
tgatactatc aaagatggca acaagattgg attcaagtgg agagaggggt accacagcat 11813
atgaaaaagc ggtagccttc agtttcttgc tgatgtattc ctggaacccg cttgttagga 11873
ggatttgcct gttggtcctt tcgcaacagc cagagacaga cccatcaaaa catgccactt 11933
attattacaa aggtgatcca ataggggct ataaagatgt aataggtcgg aatctaagt 11993
aactgaagag aacaggcttt gagaattcg caaatctaaa ccaagcctg tccacgttg 12053
gggtctggac taagcacaca agcaaaagaa taattcagga ctgtgtgccc attgggaaag 12113
aagagggcaa ctggctagtt aagcccgaca ggctgatatc cagcaaaact ggccacttat 12173
acatacctga taaaggcttt acattacaag gaaagcatta tgagcaactg cagctaagaa 12233
cagagacaaa ccggtcatg ggggttggga ctgagagata caagttaggt cccatagtca 12293
atctgtgtct gagaagggtg azaattctgc tcatgacggc cgtcggcgtc agcagctgag 12353
acaaaatgta tataattgaa ataaattaat ccatgtacat agtgcataata aatetagtgt 12413
ggaccgtcca cctcaagag atgacacgcc caacacgcac agctaacag tagtcaagat 12473
tatctacctc aagataaac tacatttat gcacacagca ctttagctgt atgaggatac 12533

11

gcccgacgtc tatagttgga ctagggaaga cctctaacag

12573

<210> 2

<211> 102

<212> PRT

<213> Bovine viral diarrhea virus

<400> 2

Ser Asp Thr Lys Glu Glu Gly Ala Thr Lys Lys Lys Thr Gln Lys Pro
 1 5 10 15

Asp Arg Leu Glu Arg Gly Lys Met Lys Ile Val Pro Lys Glu Ser Glu
 20 25 30

Lys Asp Ser Lys Thr Lys Pro Pro Asp Ala Thr Ile Val Val Glu Gly
 35 40 45

Val Lys Tyr Gln Val Arg Lys Lys Gly Lys Thr Lys Ser Lys Asn Thr
 50 55 60

Gln Asp Gly Leu Tyr His Asn Lys Asn Lys Pro Gln Glu Ser Arg Lys
 65 70 75 80

Lys Leu Glu Lys Ala Leu Leu Ala Trp Ala Ile Ile Ala Ile Val Leu
 85 90 95

Phe Gln Val Thr Met Gly
 100

<210> 3

<211> 227

<212> PRT

<213> Bovine viral diarrhea virus

<400> 3

Glu Asn Ile Thr Gln Trp Asn Leu Gln Asp Asn Gly Thr Glu Gly Ile
 1 5 10 15

Gln Arg Ala Met Phe Gln Arg Gly Val Asn Arg Ser Leu His Gly Ile
 20 25 30

Trp Pro Glu Lys Ile Cys Thr Gly Val Pro Ser His Leu Ala Thr Asp
 35 40 45

Ile Glu Leu Lys Thr Ile His Gly Met Met Asp Ala Ser Glu Lys Thr
 50 55 60

... 12

Asn Tyr Thr Cys Cys Arg Leu Gln Arg His Glu Trp Asn Lys His Gly
65 70 75 80

Trp Cys Asn Trp Tyr Asn Ile Glu Pro Trp Ile Leu Val Met Asn Arg
85 90 95

Thr Gln Ala Asn Leu Thr Glu Gly Gln Pro Pro Arg Glu Cys Ala Val
100 105 110

Thr Cys Arg Tyr Asp Arg Ala Ser Asp Leu Asn Val Val Thr Gln Ala
115 120 125

Arg Asp Ser Pro Thr Pro Leu Thr Gly Cys Lys Lys Gly Lys Asn Phe
130 135 140

Ser Phe Ala Gly Ile Leu Met Arg Gly Pro Cys Asn Phe Glu Ile Ala
145 150 155 160

Ala Ser Asp Val Leu Phe Lys Glu His Glu Arg Ile Ser Met Phe Gln
165 170 175

Asp Thr Thr Leu Tyr Leu Val Asp Gly Leu Thr Asn Ser Leu Glu Gly
180 185 190

Ala Arg Gln Gly Thr Ala Lys Leu Thr Thr Trp Leu Gly Lys Gln Leu
195 200 205

Gly Ile Leu Gly Lys Lys Leu Glu Asn Lys Ser Lys Thr Trp Phe Gly
210 215 220

Ala Tyr Ala
225

<210> 4
<211> 195
<212> PRT
<213> Bovine viral diarrhea virus

<400> 4

Ala Ser Pro Tyr Cys Asp Val Asp Arg Lys Ile Gly Tyr Ile Trp Tyr
1 5 10 15

Thr Lys Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile Val
20 25 30

Gly Pro Gly Lys Phe Gly Thr Asn Ala Glu Asp Gly Lys Ile Leu His

13

35

40

45

Glu Met Gly Gly His Leu Ser Glu Val Leu Leu Leu Ser Leu Val Val
50 55 60

Leu Ser Asp Phe Ala Pro Glu Thr Ala Ser Val Met Tyr Leu Ile Leu
65 70 75 80

His Phe Ser Ile Pro Gln Ser His Val Asp Val Met Asp Cys Asp Lys
85 90 95

Thr Gln Leu Asn Leu Thr Val Glu Leu Thr Thr Ala Glu Val Ile Pro
100 105 110

Gly Ser Val Trp Asn Leu Gly Lys Tyr Val Cys Ile Arg Pro Asn Trp
115 120 125

Trp Pro Tyr Glu Thr Thr Val Val Leu Ala Phe Glu Glu Val Ser Gln
130 135 140

Val Val Lys Leu Val Leu Arg Ala Leu Arg Asp Leu Thr Arg Ile Trp
145 150 155 160

Asn Ala Ala Thr Thr Thr Ala Phe Leu Val Cys Leu Val Lys Ile Val
165 170 175

Arg Gly Gln Met Val Gln Gly Ile Leu Trp Leu Leu Leu Ile Thr Gly
180 185 190

Val Gln Gly
195

<210> 5

<211> 374

<212> FRT

<213> Bovine viral diarrhea virus

<400> 5

His Leu Asp Cys Lys Pro Glu Phe Ser Tyr Ala Ile Ala Lys Asp Glu
1 5 10 15

Arg Ile Gly Gln Leu Gly Ala Glu Gly Leu Thr Thr Thr Trp Lys Glu
20 25 30

Tyr Ser Pro Gly Met Lys Leu Glu Asp Thr Met Val Ile Ala Trp Cys
35 40 45

14

Glu Asp Gly Lys Leu Met Tyr Leu Gln Arg Cys Thr Arg Glu Thr Arg
50 55 60

Tyr Leu Ala Ile Leu His Thr Arg Ala Leu Pro Thr Ser Val Val Phe
65 70 75 80

Lys Lys Leu Phe Asp Gly Arg Lys Gln Glu Asp Val Val Glu Met Asn
85 90 95

Asp Asn Phe Glu Phe Gly Leu Cys Pro Cys Asp Ala Lys Pro Ile Val
100 105 110

Arg Gly Lys Phe Asn Thr Thr Leu Leu Asn Gly Pro Ala Phe Gln Met
115 120 125

Val Cys Pro Ile Gly Trp Thr Gly Thr Val Ser Cys Thr Ser Phe Asn
130 135 140

Met Asp Thr Leu Ala Thr Thr Val Val Arg Thr Tyr Arg Arg Ser Lys
145 150 155 160

Pro Phe Pro His Arg Gln Gly Cys Ile Thr Gln Lys Asn Leu Gly Glu
165 170 175

Asp Leu His Asn Cys Ile Leu Gly Gly Asn Trp Thr Cys Val Pro Gly
180 185 190

Asp Gln Leu Leu Tyr Lys Gly Gly Ser Ile Glu Ser Cys Lys Trp Cys
195 200 205

Gly Tyr Gln Phe Lys Glu Ser Glu Gly Leu Pro His Tyr Pro Ile Gly
210 215 220

Lys Cys Lys Leu Glu Asn Glu Thr Gly Tyr Arg Leu Val Asp Ser Thr
225 230 235 240

Ser Cys Asn Arg Glu Gly Val Ala Ile Val Pro Gln Gly Thr Leu Lys
245 250 255

Cys Lys Ile Gly Lys Thr Thr Val Gln Val Ile Ala Met Asp Thr Lys
260 265 270

Leu Gly Pro Met Pro Cys Arg Pro Tyr Glu Ile Ile Ser Ser Glu Gly
275 280 285

15

Pro Val Glu Lys Thr Ala Cys Thr Phe Asn Tyr Thr Lys Thr Leu Lys
 290 295 300

Asn Lys Tyr Phe Glu Pro Arg Asp Ser Tyr Phe Gln Gln Tyr Met Leu
 305 310 315 320

Lys Gly Glu Tyr Gln Tyr Trp Phe Asp Leu Glu Val Thr Asp His His
 325 330 335

Arg Asp Tyr Phe Ala Glu Ser Ile Leu Val Val Val Val Ala Leu Leu
 340 345 350

Gly Gly Arg Tyr Val Leu Trp Leu Leu Val Thr Tyr Met Val Leu Ser
 355 360 365

Glu Gln Lys Ala Leu Gly
 370

<210> 6
 <211> 70
 <212> PRT
 <213> Bovine viral diarrhea virus

<400> 6

Ile Gln Tyr Gly Ser Gly Glu Val Val Met Met Gly Asn Leu Leu Thr
 1 5 10 15

His Asn Asn Ile Glu Val Val Thr Tyr Phe Leu Leu Leu Tyr Leu Leu
 20 25 30

Leu Arg Glu Glu Ser Val Lys Lys Trp Val Leu Leu Leu Tyr His Ile
 35 40 45

Leu Val Val His Pro Ile Lys Ser Val Ile Val Ile Leu Leu Met Ile
 50 55 60

Gly Asp Val Val Lys Ala
 65 70

<210> 7
 <211> 12301
 <212> LNA
 <213> Swine fever virus

<220>
 <221> CDS
 <222> (878)..(1174)
 <223> core protein

<220>
 <221> CDS
 <222> (1175)..(1855)
 <223> E-rns protein

<220>
 <221> CDS
 <222> (1856)..(2440)
 <223> E1 protein

<220>
 <221> CDS
 <222> (2441)..(3559)
 <223> E2 protein

<220>
 <221> CDS
 <222> (3560)..(3769)
 <223> p7 protein

<400> 7
 gtatacagagg ttagtgcatt ctctgtatgca tgattgggcca aatcaaaatt tcaatttgggt 60
 tcaggggcctc cctccagcga cggccgaact gggctagcca tgcccacagt aggactagca 120
 aacggaggga ctatgcgttag tggcgagctc cctgggtggt ctaagtcttg agtacaggac 180
 aqtcgtcagt agttcgacgt gaggcagaagc ccacctcgag atgctatgtg gacgagggca 240
 tgcccacagac acaccttaac cctagcgggg gtcgctaggg tgaatcaca ccacgtgatg 300
 ggagtacgac ctgatagggc gctgcagagg cccactatta ggctagtata aaaatctctg 360
 ctgtacatgg cacatggagt tgaatcattt tgaactttta tacaaaacaa acaaacaaaa 420
 eccaatggga gtggaggaa cggatataca tgccacgggg aggcatttgt ttggagaccc 480
 gagtgcagga caccacaaat ccacactgaa gctaccacat gataggggga gagglacat 540
 caaaacaaca ctgaagaacc tacctaggaa aggcgactgc aggagtgga accatctagg 600
 cccgllagl gggatatatg taaagccggg cctgtcttt tatcaggact acatgggccc 660
 ggtctaccat agagccctc tagagttttt taacgaagcg cagttttgag aggtgaccaa 720
 aaggataggt aggtgcacag gtatgcacgg aaagctttac catatatatg tgtgcacga 780
 tggttgcata ctgctgaagc tagccaagag gacgagcca agaaccctga agtggattag 840
 aaatttcacc gactgtccat tgtgggttac cagttgc tct gat gat ggc gca agt 895
 Ser Asp Asp Gly Ala Ser
 1 5
 gga agt aaa gag aag aag cca gat agg atc aac aaa ggc aaa tta aaa 913
 Gly Ser Lys Glu Lys Lys Pro Asp Arg Ile Asn Lys Gly Lys Leu Lys
 10 15 20
 ata gcc cca aaa gag cat gag aag gac agc aga act aag cca cct gag 991
 Ile Ala Pro Lys Glu His Glu Lys Asp Ser Arg Thr Lys Pro Pro Asp
 25 30 35

17

gct acg att gta gtg gaa gga gta aaa tac cag gtt aaa aag aag ggt Ala Thr Ile Val Val Glu Gly Val Lys Tyr Gln Val Lys Lys Lys Gly 40 45 50	1039
aaa gtt aaa gga aag agt acc caa gac ggc ctg tac cac aac aag aat Lys Val Lys Gly Lys Ser Thr Gln Asp Gly Leu Tyr His Asn Lys Asn 55 60 65 70	1087
aaa cca cca gaa tct agg aag aaa tta gaa aaa gcc cta ttg gca tgg Lys Pro Pro Glu Ser Arg Lys Lys Leu Glu Lys Ala Leu Leu Ala Trp 75 80 85	1135
ggg gta ata gca att atg ttg tac caa cca gtt gaa gcc gaa aat ata Ala Val Ile Ala Ile Met Leu Tyr Gln Pro Val Glu Ala Glu Asn Ile 90 95 100	1183
act caa tgg aac ctg agt gac aac ggc act aat ggt atc cag cat gct Thr Gln Trp Asn Leu Ser Asp Asn Gly Thr Asn Gly Ile Gln His Ala 105 110 115	1231
atg tac ctt aga ggg gtt agc agg agc ttg cat ggg atc tgg ccg gaa Met Tyr Leu Arg Gly Val Ser Arg Ser Leu His Gly Ile Trp Pro Glu 120 125 130	1279
aaa ata tgc aaa gga gtc ccc acc tac ctg gcc aca gac acg gaa ctg Lys Ile Cys Lys Gly Val Pro Thr Tyr Leu Ala Thr Asp Thr Glu Leu 135 140 145 150	1327
aaa gaa ata cag gga atg atg gat gcc agc gag ggg aca aac tat acg Lys Glu Ile Gln Gly Met Met Asp Ala Ser Glu Gly Thr Asn Tyr Thr 155 160 165	1375
tgc tgt aag tta cag aga cat gaa tgg aac aac cat gga tgg tgt aac Cys Cys Lys Leu Gln Arg His Glu Trp Asn Lys His Gly Trp Cys Asn 170 175 180	1423
ggg tac aat ata gac ccc tgg ata cag ttg atg aat aga acc caa gca Trp Tyr Asn Ile Asp Pro Trp Ile Gln Leu Met Asn Arg Thr Gln Ala 185 190 195	1471
aac ttg gca gaa ggc cct ccg gcc aag gag tgc gct gtg act tgc agg Asn Leu Ala Glu Gly Pro Pro Ala Lys Glu Cys Ala Val Thr Cys Arg 200 205 210	1519
tac gat aaa gat gct gac atc aac gtg gtc acc cag gcc aga aac agg Tyr Asp Lys Asp Ala Asp Ile Asn Val Val Thr Gln Ala Arg Asn Arg 215 220 225 230	1567
cca aca acc ctg acc ggt tgc aag aaa gga aaa aat ttt tct ttt gcg Pro Thr Thr Leu Thr Gly Cys Lys Lys Gly Lys Asn Phe Ser Phe Ala 235 240 245	1615
ggt aca gtt ata gag ggc cca tgt aat ttc aat gtt tcc gtg gag gat Gly Thr Val Ile Glu Gly Pro Cys Asn Phe Asn Val Ser Val Glu Asp 250 255 260	1663
atc ttg tat ggg gat cat gag tgc ggc agt ttg ctt cag gac acg gct Ile Leu Tyr Gly Asp His Glu Cys Gly Ser Leu Leu Gln Asp Thr Ala 265 270 275	1711

18

ctg tac cta gtg gat gga atg acc aac act ata gag aat gcc aga cag Leu Tyr Leu Val Asp Gly Met Thr Asn Thr Ile Glu Asn Ala Arg Gln 280 285 290	1759
gga gca gcg agg gta aca tct tgg ctc ggg agg caa ctc agc act gcc Gly Ala Ala Arg Val Thr Ser Trp Leu Gly Arg Gln Leu Ser Thr Ala 295 300 305 310	1807
ggg aag agg ttg gag ggt aga agc aaa acc tgg ttt ggt gcc tat gcc Gly Lys Arg Leu Glu Gly Arg Ser Lys Thr Trp Phe Gly Ala Tyr Ala 315 320 325	1855
cta tgg cct tac tgt aat gta aca agc aaa ata ggg tac ata tgg tac Leu Ser Pro Tyr Cys Asn Val Thr Ser Lys Ile Gly Tyr Ile Trp Tyr 330 335 340	1903
act aac aac tgc acc cgg gct tgc ctc ccc aaa aat aca aag ata ata Thr Asn Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile Ile 345 350 355	1951
ggc ccc gga aaa ttt gac act aac gcg gaa gac gga aag att ctc cat Gly Pro Gly Lys Phe Asp Thr Asn Ala Glu Asp Gly Lys Ile Leu His 360 365 370	1999
gag atg ggg ggt cac cta tca gaa ttt ctg ctg ctc tcl ctg gtt gtt Glu Met Gly Gly His Leu Ser Glu Phe Leu Leu Leu Ser Leu Val Val 375 380 385 390	2047
ctg tct gac ttc gcc cct gaa aca gcc agc gcg tta tac ctc att ttg Leu Ser Asp Phe Ala Pro Glu Thr Ala Ser Ala Leu Tyr Leu Ile Leu 395 400 405	2095
cac tac atg att cct caa tcc cat gaa gaa cct gaa ggc tgc gac aca His Tyr Met Ile Pro Gln Ser His Glu Glu Pro Glu Gly Cys Asp Thr 410 415 420	2143
aac cag ctg aat cta aca gtc gaa ctc agg act gaa gac gta ata cgg Asn Gln Leu Asn Leu Thr Val Glu Leu Arg Thr Glu Asp Val Ile Pro 425 430 435	2191
tca tca gtc tgg aat gtt gcc aac tat gtg tgt gtt aga cca gac tgg Ser Ser Val Trp Asn Val Gly Lys Tyr Val Cys Val Arg Pro Asp Trp 440 445 450	2239
tgg cca tat gaa acc aag gtg gct ttg tta ttt gaa gag gca gca cag Trp Pro Tyr Glu Thr Lys Val Ala Leu Leu Phe Glu Glu Ala Gly Gln 455 460 465 470	2287
gtc gta aaa tta gcc tta cga gcg ctg agg gat tta acc agg gtc tgg Val Val Lys Leu Ala Leu Arg Ala Leu Arg Asp Leu Thr Arg Val Trp 475 480 485	2335
aal agc gca tca aac acg gca ttc ctc atc tgc ttg ata aaa gta tta Asn Ser Ala Ser Thr Thr Ala Phe Leu Ile Cys Leu Ile Lys Val Leu 490 495 500	2383
aga gga cag atc gtg caa ggt gtg ata tgg ctg cta cta gta act ggg Arg Gly Gln Ile Val Gln Gly Val Ile Trp Leu Leu Leu Val Thr Gly 505 510 515	2431
gca caa ggc cgg cta gcc tgc aag gaa gat tac agg tac gca ata tca	2479

Ala Gln Gly Arg Leu Ala Cys Lys Glu Asp Tyr Arg Tyr Ala Ile Ser	
520 525 530	
tcg acc aat gag ata ggg cta ctc ggg gcc gaa ggt ctc acc acc acc	2527
Ser Thr Asn Glu Ile Gly Leu Leu Gly Ala Glu Gly Leu Thr Thr Thr	
535 540 545 550	
tgg aaa gaa tac aac cac gat ttg caa ctg aat gac ggg acc gtt aag	2575
Trp Lys Glu Tyr Asn His Asp Leu Gln Leu Asn Asp Gly Thr Val Lys	
555 560 565	
gcc att tgc gtg gca ggt tcc ttt aaa gtc ata gca ctt aat gtg gtc	2623
Ala Ile Cys Val Ala Gly Ser Phe Lys Val Ile Ala Leu Asn Val Val	
570 575 580	
agt agg agg tat ttg gca tca ttg cat aag gag gct tca ctc act tcc	2671
Ser Arg Arg Tyr Leu Ala Ser Leu His Lys Glu Ala Ser Leu Thr Ser	
585 590 595	
gtg aca ttt gag ctc ctg ttc gac ggg acc aac cca tca act gag gaa	2719
Val Thr Phe Glu Leu Leu Phe Asp Gly Thr Asn Pro Ser Thr Glu Glu	
600 605 610	
atg gga gat gac ttc ggg ttc ggg ctg tgc ccg ttc gat acg agt cct	2767
Met Gly Asp Asp Phe Gly Phe Gly Leu Cys Pro Phe Asp Thr Ser Pro	
615 620 625 630	
gtt gtc aag gga aag tac aat aca acc ttg ttg aac ggt agt gct ttc	2815
Val Val Lys Gly Lys Tyr Asn Thr Thr Leu Leu Asn Gly Ser Ala Phe	
635 640 645	
tat ctt gtc tgc cca ata ggg tgg acg ggt gtc ata gag tgc aca gca	2863
Tyr Leu Val Cys Pro Ile Gly Trp Thr Gly Val Ile Glu Cys Thr Ala	
650 655 660	
gtg agc cca aca act ctg aga aca gaa gtg gta aag acc ttc agg aga	2911
Val Ser Pro Thr Thr Leu Arg Thr Glu Val Val Lys Thr Phe Arg Arg	
665 670 675	
gac aag ccc ttt ccg cac aga atg gat tgt gcg acc acc aca gtg gaa	2959
Asp Lys Pro Phe Pro His Arg Met Asp Cys Ala Thr Thr Thr Val Glu	
680 685 690	
aat gga gat tta ttc tac tgt aag ttg ggg ggc aac tgg aca tgt gtg	3007
Asn Gly Asp Leu Phe Tyr Cys Lys Leu Gly Gly Asn Trp Thr Cys Val	
695 700 705 710	
aaa ggt gaa cca gtg gtc tac acg ggg ggg cta gta aza caa tgc aga	3055
Lys Gly Glu Pro Val Val Tyr Thr Gly Gly Leu Val Lys Gln Cys Arg	
715 720 725	
tgg tgt ggc ttc gac ttc aat gag ccc gac gga ctc ccg cac tac ccc	3103
Trp Cys Gly Phe Asp Phe Asn Glu Pro Asp Gly Leu Pro His Tyr Pro	
730 735 740	
ata ggt aag tgc atc ttg gta aat gag aca ggt tac aga ata gta gat	3151
Ile Gly Lys Cys Ile Leu Val Asn Glu Thr Gly Tyr Arg Ile Val Asp	
745 750 755	
tca acg gac tgt aac aga gat gcc gtt gta atc agc aca gat ggg agt	3193
Ser Thr Asp Cys Asn Arg Asp Gly Val Val Ile Ser Thr Asp Gly Ser	

760	765	770	
cat gag tgc ttg atc ggt aac aca act gtc aag gtg cat gca tca gat			3247
His Glu Cys Leu Ile Gly Asn Thr Thr Val Lys Val His Ala Ser Asp			
775	780	785	790
gaa aga ctg ggc cct atg cca tgc aga ccc aaa gag att gtc tct agt			3295
Glu Arg Leu Gly Pro Met Pro Cys Arg Pro Lys Glu Ile Val Ser Ser			
	795	800	805
gca gga cct gta agg aaa act tcc tgt aca ttc aac tac gca aaa act			3343
Ala Gly Pro Val Arg Lys Thr Ser Cys Thr Phe Asn Tyr Ala Lys Thr			
	810	815	820
ttg aag aac aag tac tat gag ccc agg gac agc tac ttc cag caa tat			3391
Leu Lys Asn Lys Tyr Tyr Glu Pro Arg Asp Ser Tyr Phe Gln Gln Tyr			
	825	830	835
atg ctt aag ggc gag tat cag tac tgg ttt gac ctg gac gtg act gac			3439
Met Leu Lys Gly Glu Tyr Gln Tyr Trp Phe Asp Leu Asp Val Thr Asp			
	840	845	850
cgc cac tca gat tac ttc gca gaa ttt gtc gtc ttg gta gtg gta gca			3487
Arg His Ser Asp Tyr Phe Ala Glu Phe Val Val Leu Val Val Val Ala			
	855	860	865
ctg tta gga gga aga tat gtc ctg tgg cta ata gtg acc tac ata gtt			3535
Leu Leu Gly Gly Arg Tyr Val Leu Trp Leu Ile Val Thr Tyr Ile Val			
	875	880	885
cta aca gaa caa ctc gcc gct ggt tta cca ttg ggc cag ggt gag gta			3583
Leu Thr Glu Gln Leu Ala Ala Gly Leu Pro Leu Gly Gln Gly Glu Val			
	890	895	900
gtg ttg ata ggg aac tta att acc cac aca gac att gag gtc gta gta			3631
Val Leu Ile Gly Asn Leu Ile Thr His Thr Asp Ile Glu Val Val Val			
	905	910	915
tat ttc tta cta ctc tat ttg gtc atg agg gat gag cct ata aag aaa			3679
Tyr Phe Leu Leu Leu Tyr Leu Val Met Arg Asp Glu Pro Ile Lys Lys			
	920	925	930
tgg ata ctg ctg ctg ttc cat ggt atg act aac aat cca gtc aag acc			3727
Trp Ile Leu Leu Leu Phe His Ala Met Thr Asn Asn Pro Val Lys Thr			
	935	940	945
ata aca gtg gca ttg ctt atg gtt agt ggg gtt gcc aag ggt			3769
Ile Thr Val Ala Leu Leu Met Val Ser Gly Val Ala Lys Gly			
	955	960	
gcgaagatag acggcggttg gcagcggttg ccagagacca gctttgacat ccaactcgcg			3829
ctgacagtta tagtagtcgc tgtgatgcta ctggcaaaaga gagatccaac tactgtcccc			3889
ttggttataa cagtggcaac cctgagaaag gctaagatga ctaatggact tagcacggat			3943
atagccatag ctacagtgtc aacagcgttg ctaacctgga cctacattag tgactattat			4003
agatacaaga cttggctaca gtacctattt agcacagtga caggtatctt cttaataagg			4063
gtactgaagg gaataggtag gttggattta cacactccaa ccttgccatc ctacagaccc			4129

ctctctcttca ttctcgtgta cctcatttcc actgcagtg taacaagatg gaattctggac 4189
atagccggat tgctgttgca gtgtgtccca acccttttga tggtttttac gatgtgggca 4249
gacatttctca cctgatcct catactgccc acttacgagc taacaaaaact atattacctc 4309
aagggaagtga agactgggyc agaaaagggc tggttatgga agaccaactt caagaggqta 4369
aacgacatat acgaagttga ccaatctggt gaagggttt accctttccc gtcaaaaaca 4429
aagacaagtt caataacagg taccatgttg ccattgatca aagccatact catcagctgc 4489
alcagtaata aqtgcagtt catatatcta ttgtacttga tatttgaact qtcttactac 4549
ctccacaaga agatcataga tgaatagca ggagggaaca acttcacttc aagacttcta 4609
gocgcttga tgaagocaa ttgggccttt gacaacgaag aaqtagggg ttlaaqaag 4669
lcttccctgt tctctagtga ggttaagaa ctgatcatca aacacaaagt gaggaatgaa 4729
gtaatggtcc actggtttg tgacgaagag gtttatggga tgccaaagt gggtggctta 4789
gtcaaggcag caacattgag taaaaataa cattgtattt tgtgcaccgt ctgtgaagac 4849
agagagtga gaggaagaac ctgccccaaa tgcgggcgtl ttgggccacc aatgaacctg 4909
ggtatgacc tagccgactt tgaagaaaaa cattataaga ggtcttttt tagagaggat 4969
caatcagaag ggccggttag agaggagtac gcagggtatc tgcaatatac agccagagg 5029
caattattcc tgaggaaatc cccggtgcta gcaacaaaag tcaagatgct cctggtcgg 5089
aatcttggga cggaggtgg agacttggaa caocttggct gggtccttag ggggcctgcc 5149
gtttgcaaga aggttaccga acatgagaaa tgcaccacat ccataatgga caaattgact 5209
gcttttttcg gtgttatgcc aaggggcacc acacctagag cccctgtgag attccccacc 5269
tctctcttaa agataagaag ggggttggaa actggctggg cgtacacaca ccaaggtggc 5329
attagttcag tggacctgt cacttgtggg aaagacttgc tggtatgta cactatgggc 5389
cggacaaggg tcttttgcca atcaataat aagatqacag atgaghtga gtatggagtt 5449
aaaactgact ccggatgccc ggaaggaggt aggtgttatg tglcaaccc agaggcagtt 5509
aacatctcag gactaaagc agccatggtc cacttacaaa aaactggagg agaattcacc 5569
tgtgtgacag catcaggaac tccggccttc ttgaltca agaacctcaa aggtgtgtca 5629
gggtaccca tatttgagc atcaagtga agggtagtcg gcagggtcaa ggtcgggaag 5689
aatgaggact ctaaaccaac caagcttatg agtggaaac aaacagltc caaagttacc 5749
acagacttga cagaaaggt aagaaatac acgacctga acgggggagz attcagacca 5809
atacccttg ctacaggtgc cggaaaacc acggaactcc ctgggtcagt catagaagag 5869
atagggagc ataagaggt ctgggtcttg atccctctga ggggggcagc agautcagta 5929

taccaatata tgagacaaaa acatccaagc atcgcattha acctgaggat aggggagatg 5989

aaggaagggg acatggccac agggataacc tatgcttcat acggttactt ctgtcagatg 6049

ccacaaccta agttgcgagc cgcgatggtt gagtactcct tcataatttct tgacgagtac 6109

cactgtgcca cccagaaca attggccatc atgggaaaga tccacagatt ttcagagaac 6169

ctgcgggttag tagccatgac cgcaacacca gcaggcacag taacaaccac agggcagaaa 6229

cacctatag aagaattcat agccccagaa gtgatgaaag gggaagactt aggtcagag 6289

tacttggaaca ttgctggact aaagatacca gtagaggaga tgaagagcaa catgctggtt 6349

tttgtgcca ctaggaaatc ggcgggtggag acagcaaaga aattgaaagc taagggttac 6409

aactcaggct actattatag tggagaggat ccattctaacc tgagggtggt aacgtcgag 6469

tcccgtacg tgggtggtggc aaccaacgag atagaatcag gtgttactct ccggacttg 6529

gatgtggttg tgatacagg gcttaagtgt gaaagagaa tacggctgtc acctaatg 6589

cccttcctag tgacgggcct gaagagaatg gctgtcacga ttggggaaca agcccagaga 6649

agggggagag ttgggagagt aaagcctggg agatactaca ggagtcaaga aactccggtt 6709

ggttctaaag attaccatta tgatctactg caagcacaga ggtacggtat tgaagatggg 6769

ataaacatca ccaaatcctt tagagagatg aactatgatt ggagccttta tgaggaggac 6829

agtctgatga ttacacaatt ggaatcctc aataatttgt tgatatcaga agaactaccg 6889

atggcagtaa aaaatataat ggccaggact gaccaccag aaccaattca gctggcgtag 6949

aacagctacg aaacacaagt gccagtgcta ttcccaaaaa taaagaatgg agaggtagct 7009

gatagttacg ataactatac ctctctcaac gcaagaaaat tgggggatga tgtacccct 7069

tacgtgtatg ccacagagga tgaggactta gcggtagagc tactgggctt agactggcca 7129

gacctggaa accaaggaa cgtagaggct ggagagcac taaaacaagt agttggtcta 7189

tcaacagctg agaatgcctt gttagtagcc ttattcggct atgtaggata tcaggcactt 7249

tcaaagaggc atataccagt agtcacagat atatattcaa ttgaagatca caggttggaa 7309

gacaccacac acctacagta cgtcccaaat gctatcaaga cggaggggaa ggagacagaa 7369

ttgaaggagc tagccagggg gcatgtgcag agatgtgtgg aagctatgac caattatgca 7429

agagagggta tccaattcat gaagtctcag gcactgaagg tgaagaaac cccacttac 7489

aaagagacaa tgaactctgt gactgactat gtaaaagaaat tcatggaggc gctggcagac 7549

agtaagagag acatctcaag atatgggttg tgggggacgc acacagcctt atataagagc 7609

atcagtcca ggcctgggag tgagactgcg ttctctaccc tggctgtgaa gtggtggca 7669

tttggggggg aatcaatagc agacctgtc aaacaagcgg ccacagactt ggtcgtctac 7729

tatatcatca acagacctca gttccagga gacacagaga cacaacagga aggaaggaaa 7789

tttgtggcca gctactcgt ctcagctcta gctacttaca catacaaaaag ctggaattac 7849
 aataatctgt ccaagatagt tgaacgggt ttggccactc tgccttatgc cgcacagct 7909
 ctcaaaactat tcgccccac tcgattggag agcgttgta tattgagtac cgcaatctac 7969
 aagacctacc tatcaatcag ggcgggaaaa agcgttggt tgctaggcac aggggttagt 8029
 ggggttatgg agatcatgt acaaaatcca gtatccgtgg gcatagcagt catgctaggg 8089
 gtaggggcgg tggcagccca caatcgaac gagccagtg agcagaagag aacactactc 8149
 atgaaagtgt ttgtaaaaga cttcttgga caagcagcca ctgatgaatt agtcaaggag 8209
 agtcttgaga aaataataat ggcttgttt gaagcagtg agacagtgg taacctctt 8269
 agactagtat accacctta tggagttttc tataaggggt gggaggcaaa agagttggcc 8329
 caaaggacag ccggtaggaa ctttttact ttgataatgt tcgaggctgt ggaactactg 8389
 ggagtagata gtgaaggaaa gatccgcag ctatcaagta attacatact agagctctg 8449
 tataagttcc gtgacgtat caagtctagc gtgagggaqa tggcaatcag ctgggcccct 8509
 gcccccttca gctgtgattg gacacgcagc gatgacagaa tagggctccc ccagacaaat 8569
 ttctccaag tggagacgaa atgcccctgt ggttacaaga tgaaggcagt taagaattgt 8629
 gctggagagc tgagactctt ggaggaggaa ggctcatttc tctgcagaa taaattcggg 8689
 agaggttcac ggaactacag ggtgacaaaa tactatgatg acaatctatc agaataaag 8749
 ccagtataa gaatggaag gcatgtgaa ctctactaca agggagccac catcaaatg 8809
 gacttcaaca acagtaaac aatactggca accgataaat gggagattga tcactccact 8869
 ctggtcaggg tgctcaagag gcacacaggg gctggatata atggggcata cctgggcgaq 8929
 aaaccgaact acaaacatct gatagagag gactgtgca ccatcaccac agataaggtt 8989
 tgttttctca aaatgaagag aggggtgtga tttacttatg acttatccct tcacaacctt 9049
 acccgactga ttgaattggt acacagaaat aacttggag acaaagagat tctgtctgtt 9109
 acgcttaca cctggctggc ttacacgttt gtaaalgaag atataggga cataaaacca 9169
 gcttcgggg agaaagtaac accggagatg caggaggaaa taaccttga gctgtctga 9229
 gtggtggata caactgact gaccgtgact gtggtagggg aagccccac tatgactaca 9289
 gggagactc cgcagcgtt caccagctca gtttcagacc cgaagggca acaagtttta 9349
 aaactgggg tgggtgaag ccaatcccc gggactaat cccagagggc aagcctgcac 9409
 gaagccatc aaggtgcaga tgagagacc tcgggtgctga tattagggtc tgataaagcc 9469
 accttaata ggtgaaaac tgcaagaal gtaaaagtal acagaggcag ggaacccaca 9529
 gaagtgaag atatgatgag gaggggaaa atcctggta tagccctgtc taggggtgat 9589

aatgctctat tgaaatttgt tgactacaaa ggcaccttct taactagaga gaccttagag 9649
gcattaagtt tgggtaggcc taaaaagaaa aacataacca aggcagaagc gcagtgggtg 9709
ctgtgectcg aagaccaa at ggaagagcta cccgatttgt tcgcagccgg ggaacccatt 9769
ttcttagagg ctaacattaa acatgacagg taccatctgg tgggggatat agctaatact 9829
aaggaaaaag ccaacagtt gggagctaca gactccacaa agatatctaa ggaggtttgt 9889
gcaaaagtgt attctatgaa actgagtaat tgggtgatgc aagaagaaaa taaacagggc 9949
aacctgaccc ccttgtttga agagctcctg caacagtgt caccggagg ccagaacaaa 10009
actgcacata tggctctctg ttaccaacta gctcaaggga actggatgcc aaccagctgc 10069
catgrrttta tggggaccat atctgccagg aggaccaaga cccatccata tgaagcatac 10129
gtcaagttaa gggagtgtgt agaggaacac aagatgaaaa cattgtgtcc tggatcaagc 10189
ctgggtaagc acaacgaatg gataatttgt aaaatcaaat accagggaaa cctgaggacc 10249
aaacacatgt tgaaccccg caaggtggca gagcaactgt gcagagagg acacagacac 10309
aatgtgtata acaagacaat aggtctagta atgacagcta ctggatcag gttggagaag 10369
ttgccgtgg ttagggccca gacagacaca accaacttcc accaagcaat aagggataag 10429
atagacaagg aagagaacct acaaaccctg ggtttacata agaaactaat ggaagttttc 10489
aatgcattga aacgaccga gttagagtcc tctacgatg ccgtggaatg ggaggaaactg 10549
gagagaggaa taaacaggaa ggggtgctgt ggtttctttg aacgcaaaa tataggggaa 10609
atattggatt cagagaaaaa caagctcga gagattattg acaatctgaa aaaaggcaga 10669
aacatcaaat actatgaaac cgcgatccca aagaatgaga agagggacgt caatgatgac 10729
tggactgctg gtgacttctg ggaagagaag aaaccacag ctatacaata cctgaagca 10789
aaaacaaggc tggccatcac caaggtgatg tataagtggg tgaagcagaa gccagtgtt 10849
ataccgggt atgaaggga gacacctcta ttccaaattt ttgacaaagt aaagaaggaa 10909
tgggatcaat tccaaaatcc agtggcagt agttttgaca ctaaggcgtg ggacaccag 10969
gtaaccacaa aagatttga gttgataaag gacatacaaa agtactattt caagaagaaa 11029
tggcataaat ttattgacac cctgaccatg cacatgtcag aagtaccgt aatcagtgt 11089
gatggggaag tatacataag gaaagggaag agaggcagt gacaacctga cacaagcgca 11149
ggcaatagca tgcataatgt gtaacaatg atttacgct tctgcaggc cacgggagta 11209
cctacaaaga gcttcgacag ggtggcaaaa attcatgtgt gtgggatga tggtttctg 11269
atcacagaaa gagctctcgg tgagaaattc gcgagtaagg gagtccagat cctatatgaa 11329
gctgggaagc ccagaagat cactgaagg gacaagatga aagtggccta ccaatttgat 11389
gatattgagt ttgctccc tacaccaata caagtaagg ggtcagata cacttctagt 11449

tacatgccgg ggagaaatac aaccacaatc ctggctaaaa tggccacaag gttagattcc 11509
 agtgggtgaga ggggtaccat agcatatgag aaagcagtag cattcagctt cctgctgatg 11569
 tactcctgga acccactaat cagaaggatc tgcttactgg tgctatcaac tgaactgcaa 11629
 gtgaaaccag ggaagtcaac cacttactac tatgaagggg acccgataac tgccatacaag 11689
 gaagtcatcg gccacaatct ttttgatctt aagagaacaa gcttcgagaa gctggccaag 11749
 ttaaattctca gcatgtcagt actcggagcc tggactagac acaccagtaa aagactacta 11809
 caagactgtg tcaatgtggg tgttaaagag ggcaactggc tagttaatgc agatagacta 11869
 gtaagtagca agactggaag taggtacata cccggagagg gccacaccct gcaagggaga 11929
 cattatgaag aactggtgtt ggcaagaaaa cagatcaaca actttcaagg gaccgacagg 11989
 tacaatctag gcccaatagt caatatgggt ttaaggaggc tgagagtcac gatgatgacc 12049
 ctgataggga gagggggtatg agcggggga acccgggac tggaccggcc agtagaacc 12109
 tgttgtagat aacactaatt tttttttatt tatttagata ttactattta tttattttt 12169
 tattttattga atgagtaaga actggtacaa actacctcaa gttaccacac tacactcatt 12229
 tttaacagca ctttagctgg aaggaaaatt cctgacgtcc acagttggac taaggtaatt 12289
 tccataacggc cc 12301

<210> 8
 <211> 99
 <212> FRT
 <213> Swine fever virus

<400> 8

Ser Asp Asp Gly Ala Ser Gly Ser Lys Glu Lys Lys Pro Asp Arg Ile
 1 5 10 15

Asn Lys Gly Lys Leu Lys Ile Ala Pro Lys Glu His Glu Lys Asp Ser
 20 25 30

Arg Thr Lys Pro Pro Asp Ala Thr Ile Val Val Glu Gly Val Lys Tyr
 35 40 45

Gln Val Lys Lys Lys Gly Lys Val Lys Gly Lys Ser Thr Gln Asp Gly
 50 55 60

Leu Tyr His Asn Lys Asn Lys Pro Pro Glu Ser Arg Lys Lys Leu Glu
 65 70 75 80

Lys Ala Leu Leu Ala Trp Ala Val Ile Ala Ile Met Leu Tyr Gln Pro
 85 90 95

Val Glu Ala

<210> 9
 <211> 227
 <212> PRT
 <213> Swine fever virus
 <400> 9

Glu Asn Ile Thr Gln Trp Asn Leu Ser Asp Asn Gly Thr Asn Gly Ile
 5 10 15

Gln His Ala Met Tyr Leu Arg Gly Val Ser Arg Ser Leu His Gly Ile
 20 25 30

Trp Pro Glu Lys Ile Cys Lys Gly Val Pro Thr Tyr Leu Ala Thr Asp
 35 40 45

Thr Glu Leu Lys Glu Ile Gln Gly Met Met Asp Ala Ser Glu Gly Thr
 50 55 60

Asn Tyr Thr Cys Cys Lys Leu Gln Arg His Glu Trp Asn Lys His Gly
 65 70 75 80

Trp Cys Asn Trp Tyr Asn Ile Asp Pro Trp Ile Gln Leu Met Asn Arg
 85 90 95

Thr Gln Ala Asn Leu Ala Glu Gly Pro Pro Ala Lys Glu Cys Ala Val
 100 105 110

Thr Cys Arg Tyr Asp Lys Asp Ala Asp Ile Asn Val Val Thr Gln Ala
 115 120 125

Arg Asn Arg Pro Thr Thr Leu Thr Gly Cys Lys Lys Gly Lys Asn Phe
 130 135 140

Ser Phe Ala Gly Thr Val Ile Glu Gly Pro Cys Asn Phe Asn Val Ser
 145 150 155 160

Val Glu Asp Ile Leu Tyr Gly Asp His Glu Cys Gly Ser Leu Leu Gln
 165 170 175

Asp Thr Ala Leu Tyr Leu Val Asp Gly Met Thr Asn Thr Ile Glu Asn
 180 185 190

Ala Arg Gln Gly Ala Ala Arg Val Thr Ser Trp Leu Gly Arg Gln Leu
195 200 205

Ser Thr Ala Gly Lys Arg Leu Glu Gly Arg Ser Lys Thr Trp Phe Gly
210 215 220

Ala Tyr Ala
225

<210> 10
<211> 195
<212> PRT
<213> Swine fever virus

<400> 10

Leu Ser Pro Tyr Cys Asn Val Thr Ser Lys Ile Gly Tyr Ile Trp Tyr
1 5 10 15

Thr Asn Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile Ile
20 25 30

Gly Pro Gly Lys Phe Asp Thr Asn Ala Glu Asp Gly Lys Ile Leu His
35 40 45

Glu Met Gly Gly His Leu Ser Glu Phe Leu Leu Leu Ser Leu Val Val
50 55 60

Leu Ser Asp Phe Ala Pro Glu Thr Ala Ser Ala Leu Tyr Leu Ile Leu
65 70 75 80

His Tyr Met Ile Pro Gln Ser His Glu Glu Pro Glu Gly Cys Asp Thr
85 90 95

Asn Gln Leu Asn Leu Thr Val Glu Leu Arg Thr Glu Asp Val Ile Pro
100 105 110

Ser Ser Val Trp Asn Val Gly Lys Tyr Val Cys Val Arg Pro Asp Trp
115 120 125

Trp Pro Tyr Glu Thr Lys Val Ala Leu Leu Phe Glu Glu Ala Gly Gln
130 135 140

Val Val Lys Leu Ala Leu Arg Ala Leu Arg Asp Leu Thr Arg Val Trp
145 150 155 160

Asn Ser Ala Ser Thr Thr Ala Phe Leu Ile Cys Leu Ile Lys Val Leu
165 170 175

Arg Gly Gln Ile Val Gln Gly Val Ile Trp Leu Leu Leu Val Thr Gly
 180 185 190

Ala Gln Gly
 195

<210> 11
 <211> 373
 <212> PRT
 <213> Swine fever virus
 <400> 11

Arg Leu Ala Cys Lys Glu Asp Tyr Arg Tyr Ala Ile Ser Ser Thr Asn
 1 5 10 15

Glu Ile Gly Leu Leu Gly Ala Glu Gly Leu Thr Thr Thr Trp Lys Glu
 20 25 30

Tyr Asn His Asp Leu Gln Leu Asn Asp Gly Thr Val Lys Ala Ile Cys
 35 40 45

Val Ala Gly Ser Phe Lys Val Ile Ala Leu Asn Val Val Ser Arg Arg
 50 55 60

Tyr Leu Ala Ser Leu His Lys Glu Ala Ser Leu Thr Ser Val Thr Phe
 65 70 75 80

Glu Leu Leu Phe Asp Gly Thr Asn Pro Ser Thr Glu Glu Met Gly Asp
 85 90 95

Asp Phe Gly Phe Gly Leu Cys Pro Phe Asp Thr Ser Pro Val Val Lys
 100 105 110

Gly Lys Tyr Asn Thr Thr Leu Leu Asn Gly Ser Ala Phe Tyr Leu Val
 115 120 125

Cys Pro Ile Gly Trp Thr Gly Val Ile Glu Cys Thr Ala Val Ser Pro
 130 135 140

Thr Thr Leu Arg Thr Glu Val Val Lys Thr Phe Arg Arg Asp Lys Pro
 145 150 155 160

Phe Pro His Arg Met Asp Cys Ala Thr Thr Thr Val Glu Asn Gly Asp
 165 170 175

29

Leu Phe Tyr Cys Lys Leu Gly Gly Asn Trp Thr Cys Val Lys Gly Glu
180 185 190

Pro Val Val Tyr Thr Gly Gly Leu Val Lys Gln Cys Arg Trp Cys Gly
195 200 205

Phe Asp Phe Asn Glu Pro Asp Gly Leu Pro His Tyr Pro Ile Gly Lys
210 215 220

Cys Ile Leu Val Asn Glu Thr Gly Tyr Arg Ile Val Asp Ser Thr Asp
225 230 235 240

Cys Asn Arg Asp Gly Val Val Ile Ser Thr Asp Gly Ser His Glu Cys
245 250 255

Leu Ile Gly Asn Thr Thr Val Lys Val His Ala Ser Asp Glu Arg Leu
260 265 270

Gly Pro Met Pro Cys Arg Pro Lys Glu Ile Val Ser Ser Ala Gly Pro
275 280 285

Val Arg Lys Thr Ser Cys Thr Phe Asn Tyr Ala Lys Thr Leu Lys Asn
290 295 300

Lys Tyr Tyr Glu Pro Arg Asp Ser Tyr Phe Gln Gln Tyr Met Leu Lys
305 310 315 320

Gly Glu Tyr Gln Tyr Trp Phe Asp Leu Asp Val Thr Asp Arg His Ser
325 330 335

Asp Tyr Phe Ala Glu Phe Val Val Leu Val Val Val Ala Leu Leu Gly
340 345 350

Gly Arg Tyr Val Leu Trp Leu Ile Val Thr Tyr Ile Val Leu Thr Glu
355 360 365

Gln Ile Ala Ala Gly
370

<210> 12
<211> 70
<212> PRT
<213> Swine fever virus

<400> 12

Leu Pro Leu Gly Gln Gly Glu Val Val Leu Ile Gly Asn Leu Ile Thr
1 5 10 15

His Thr Asp Ile Glu Val Val Val Tyr Phe Leu Leu Leu Tyr Leu Val
 20 25 30

Met Arg Asp Glu Pro Ile Lys Lys Trp Ile Leu Leu Leu Phe His Ala
 35 40 45

Met Thr Asn Asn Pro Val Lys Thr Ile Thr Val Ala Leu Leu Met Val
 50 55 60

Ser Gly Val Ala Lys Gly
 65 70

<210> 13
 <211> 12333
 <212> DNA
 <213> Border disease virus

<220>
 <221> CDS
 <222> (877)..(1176)
 <223> core protein

<220>
 <221> CDS
 <222> (1177)..(1857)
 <223> E-rns protein

<220>
 <221> CDS
 <222> (1858)..(2442)
 <223> E1 protein

<220>
 <221> CDS
 <222> (2443)..(3561)
 <223> E2 protein

<220>
 <221> CDS
 <222> (3562)..(3771)
 <223> p7 protein

<400> 13
 gtatacggga gtagctcatg cccgtataca aaattggata ttccaaaact cgattgggtt 60
 agggagccct cctagcgcag gccgaaccgt gttaaccata cagtagtag gactagcaga 120
 cggcaggact agccatcgtg gtgagatccc tgagcagttt aaatcctgag tacaggatag 180
 tgcgcagtag ttcaacgcag gcacggttct gccttgagat gctacgtgga cgagggcatg 240
 cccaagactt gctttaatct cggcgggggt cgcgcagggtg azaacaccta acggtgttgg 300
 ggttacagcc tgatagggtg ctgcagaggc ccacgaatag gctagtataa aaatctctgc 360

tgtacatggc acatggagtt gaacaagttt gaacttttat acaaaacaag taacacaaaa	420
ccagtggggg tgactgaacc tatctagac tcagcgggta accccatata tggatgaaga	480
agcacaatac acccgcagtc taccttgaaa ctaccacatg agagaggagt ggcagaagtc	540
gtaacgacac tgagagatct accaaagaaa ggtgactgca gaagtgggaa ccacgcaggt	600
ccagtaagtg ccatatatat caaacccaggc ccagtcctct accaggatta caaggggcct	660
gtataccata gagcaccact ggaacttttt gttgagacgc aattctgtga agtcacaaag	720
aquataggga gagtgaactg tagtgacggc aggcctttatc acttgatcat ttgctccgat	780
gggtgcaccc tattgaaaac agcaagtaag acaaggagtg cagtattaaa gtggacacgt	840
aatatccttg actgcccact gtgggtgaca agtggc tct gat gac aac aag agc	894
Ser Asp Asp Asn Lys Ser	
1 5	
gaa aag acy aat gag aaa aaa cca gat aga gtc agg cgg gga gcc atg	942
Glu Lys Thr Asn Glu Lys Lys Pro Asp Arg Val Arg Arg Gly Ala Met	
10 15 20	
aag atc aca ccc aag gag agt gag aag gat agt aga tct aag cca cct	990
Lys Ile Thr Pro Lys Glu Ser Glu Lys Asp Ser Arg Ser Lys Pro Pro	
25 30 35	
gac gca act ata gta gta gaa ggc ata aaa tac cag gta aag aag aag	1038
Asp Ala Thr Ile Val Val Glu Gly Ile Lys Tyr Gln Val Lys Lys Lys	
40 45 50	
gga aag gtg aag ggc aag aac aca caa gat ggc tta tac cac aac aag	1086
Gly Lys Val Lys Gly Lys Asn Thr Gln Asp Gly Leu Tyr His Asn Lys	
55 60 65 70	
aac aag cca cct gag tct aga aag aan ttg gag aac ccc cta ctg gct	1134
Asn Lys Pro Pro Glu Ser Arg Lys Lys Leu Glu Lys Ala Leu Leu Ala	
75 80 85	
tgg gct ata ata gca atc ttc atg tgg gaa ccc gta gca cca gag aat	1192
Trp Ala Ile Ile Ala Ile Phe Met Trp Glu Pro Val Ala Pro Glu Asn	
90 95 100	
gtg aca caa tgg aac cta agt gac aac ggg act acc ggc atc caa ctc	1230
Val Thr Gln Trp Asn Leu Ser Asp Asn Gly Thr Thr Gly Ile Gln Leu	
105 110 115	
cta atg ttc caa aga ggt gtt aac aga agc ctg cac ggt att tgg cct	1278
Leu Met Phe Gln Arg Gly Val Asn Arg Ser Leu His Gly Ile Trp Pro	
120 125 130	
gaa aag ata tgt aca gga glg ccc acg cac ttg gca aca gat gca gag	1326
Glu Lys Ile Cys Thr Gly Val Pro Thr His Leu Ala Thr Asp Ala Glu	
135 140 145 150	
ttg aag gga att caa ggg atg atg gat gct agt gaa aag act aat tac	1374
Leu Lys Gly Ile Gln Gly Met Met Asp Ala Ser Glu Lys Thr Asn Tyr	
155 160 165	

32

aca tgc tgc aga ctt cag aga cac gaa tgg aac aag tac ggg tgg tgc 1422
 Thr Cys Cys Arg Leu Gln Arg His Glu Trp Asn Lys Tyr Gly Trp Cys
 170 175 180

aac tgg tac aac ata aat cca tgg ata tgg ttg atg aac aag aca caa 1470
 Asn Trp Tyr Asn Ile Asn Pro Trp Ile Trp Leu Met Asn Lys Thr Gln
 185 190 195

gcc aat ctg acg gaa gga cct cca gaa aaa gaa tgc gct gtg acc tgt 1518
 Ala Asn Leu Thr Glu Gly Pro Pro Glu Lys Glu Cys Ala Val Thr Cys
 200 205 210

agg ttc gat aag gaa gca gat ata aat ata gtg aca cag gct agg gac 1566
 Arg Phe Asp Lys Glu Ala Asp Ile Asn Ile Val Thr Gln Ala Arg Asp
 215 220 225 230

agg cca aca act tta aca ggg tgt aag aaa gga aaa aaa ttt tca ttt 1614
 Arg Pro Thr Thr Leu Thr Gly Cys Lys Lys Gly Lys Lys Phe Ser Phe
 235 240 245

gct ggc atg ata att gag ggc cct tgc aac ttc aat gta tca gtg gaa 1662
 Ala Gly Met Ile Ile Glu Gly Pro Cys Asn Phe Asn Val Ser Val Glu
 250 255 260

gat ata tta ttc gga gac aat gag tgt agt agc tta ttc cag gac aca 1710
 Asp Ile Leu Phe Gly Asp Asn Glu Cys Ser Ser Leu Phe Gln Asp Thr
 265 270 275

gct ctc tac gtg gta gat gga gta acc aac acc gta gaa aat gct agg 1758
 Ala Leu Tyr Val Val Asp Gly Val Thr Asn Thr Val Glu Asn Ala Arg
 280 285 290

caa ggg gct gca aaa ttg aca tcc tgg cta ggg aag caa ttg ggt ata 1806
 Gln Gly Ala Ala Lys Leu Thr Ser Trp Leu Gly Lys Gln Leu Gly Ile
 295 300 305 310

atg ggg aaa aaa tta gaa cac aag agt aaa acg tgg ttc gca gcc aat 1854
 Met Gly Lys Lys Leu Glu His Lys Ser Lys Thr Trp Phe Gly Ala Asn
 315 320 325

gca caa tca cct tac tgt aat gta aca aga aaa ata ggg tac gtc tgg 1902
 Ala Gln Ser Pro Tyr Cys Asn Val Thr Arg Lys Ile Gly Tyr Val Trp
 330 335 340

tac aca aac aat tgc acc cct gct tgc ctc cca aag aat aca aaa ata 1950
 Tyr Thr Asn Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile
 345 350 355

ata ggt ccg ggg aaa ttt gac acc aat gcg gag gat gga aag atc ttg 1998
 Ile Gly Pro Gly Lys Phe Asp Thr Asn Ala Glu Asp Gly Lys Ile Leu
 360 365 370

cat gag atg agg ggt cat ata tgg gaa ttc att cta cta tct ttg gta 2046
 His Glu Met Arg Gly His Ile Ser Glu Phe Ile Leu Leu Ser Leu Val
 375 380 385 390

gtg cta tca gac ttc gca cct gaa aca gct agt act ctc tac ctg gtg 2094
 Val Leu Ser Asp Phe Ala Pro Glu Thr Ala Ser Thr Leu Tyr Leu Val
 395 400 405

cta cat ttt gcc tta cct caa acc cac gaa gtt cct agt gta tgt gac 2142

33

Leu His Phe Ala Leu Pro Gln Thr His Glu Val Pro Ser Val Cys Asp
 410 415 420
 acc aac caa cta aat ctt acg gtc agc ttg aga gtg gat gac gtg ata 2190
 Thr Asn Gln Leu Asn Leu Thr Val Ser Leu Arg Val Asp Asp Val Ile
 425 430 435
 cca tct tca gta tgg aac ctg gga aaa tat gtc tgt gtt aga cca gac 2238
 Pro Ser Ser Val Trp Asn Leu Gly Lys Tyr Val Cys Val Arg Pro Asp
 440 445 450
 tgg tgg ccc tat gaa aca acc atg gta ttg ttg ttt gaa gag gca gga 2286
 Trp Trp Pro Tyr Glu Thr Thr Met Val Leu Leu Phe Glu Glu Ala Gly
 455 460 465 470
 caa gta gtg aag ttg gta cta agg gcc ata agg gac ttg aca agg gtc 2334
 Gln Val Val Lys Leu Val Leu Arg Ala Ile Arg Asp Leu Thr Arg Val
 475 480 485
 tgg aac agt gca tca aca aca gcc ttt ctt ata tgc cta gtt aag gtg 2382
 Trp Asn Ser Ala Ser Thr Thr Ala Phe Leu Ile Cys Leu Val Lys Val
 490 495 500
 tta aga ggc cag gta gta cag gga cta qtg tgg cta tta ctg gta act 2430
 Leu Arg Gly Gln Val Val Gln Gly Leu Val Trp Leu Leu Leu Val Thr
 505 510 515
 ggt gca caa ggg cag ttt gct tgt aga gaa gac tac agg tat gct tta 2478
 Gly Ala Gln Gly Gln Phe Ala Cys Arg Glu Asp Tyr Arg Tyr Ala Leu
 520 525 530
 gca aga aca aag gaa ata ggg gcc ctg ggt gca gag agc ttg aca acg 2526
 Ala Arg Thr Lys Glu Ile Gly Ala Leu Gly Ala Glu Ser Leu Thr Thr
 535 540 545 550
 acc tgg act gac tac cga gga aac cta gaa ctg gac gat gga act gtg 2574
 Thr Trp Thr Asp Tyr Arg Gly Asn Leu Glu Leu Asp Asp Gly Thr Val
 555 560 565
 agg gcc aca tgt tgc aga ggt ttc ttt agg ttt aga gga cat tgc atg 2622
 Arg Ala Thr Cys Ser Arg Gly Phe Phe Arg Phe Arg Gly His Cys Met
 570 575 580
 ata ggg ccc agg tac ctg gct agc cta cac ctg agg gct cta ccc aca 2670
 Ile Gly Pro Arg Tyr Leu Ala Ser Leu His Leu Arg Ala Leu Pro Thr
 585 590 595
 tct gtc acc ttt gaa cta ata cca gga ggg tca gcg atg aca gaa gag 2718
 Ser Val Thr Phe Glu Leu Ile Pro Gly Gly Ser Ala Met Thr Glu Glu
 600 605 610
 gaa atg ggt gac gac ttt gaa ttc ggc ctg tgc cct tgl gat tct aga 2766
 Glu Met Gly Asp Asp Phe Glu Phe Gly Leu Cys Pro Cys Asp Ser Arg
 615 620 625 630
 ccc gtt gtt aag gga aaa tac aac acc act ctg ctc aac gga agt gcg 2814
 Pro Val Val Lys Gly Lys Tyr Asn Thr Thr Leu Leu Asn Gly Ser Ala
 635 640 645
 ttc caa cta ata tgc cct tac gga tgg gtc gga cgc gtg gag tgc act 2862
 Phe Gln Leu Ile Cys Pro Tyr Gly Trp Val Gly Arg Val Glu Cys Thr

650	655	660	
act gta agc aag agc acc ctg gca aca gag gtg gta aag ata tac aaa Thr Val Ser Lys Ser Thr Leu Ala Thr Glu Val Val Lys Ile Tyr Lys 665	670	675	2910
aag aca aaa cca ttt cca cag cgg gtt ggt tgc gac cac acc acc gtc Lys Thr Lys Pro Phe Pro Gln Arg Val Gly Cys Asp His Thr Thr Val 680	685	690	2958
tac aaa caa gac ctg tac cat tgc cag atg gga ggt aac tgg acg tgc Tyr Lys Gln Asp Leu Tyr His Cys Gln Met Gly Gly Asn Trp Thr Cys 695	700	705	3006
atg aga ggt gaa gta gtc aaa tat gtg ggg ggt cca gta aag aag tgt Met Arg Gly Glu Val Val Lys Tyr Val Gly Gly Pro Val Lys Lys Cys 715	720	725	3054
gag tgg tgc ggc tac gtg ttt aag aag aga gag ggt ctc cca cac tat Glu Trp Cys Gly Tyr Val Phe Lys Lys Arg Glu Gly Leu Pro His Tyr 730	735	740	3102
cca att ggt agg tgt atg cta aga aac gag act ggt tac aga agc gtg Pro Ile Gly Arg Cys Met Leu Arg Asn Glu Thr Gly Tyr Arg Ser Val 745	750	755	3150
gat gac aca cca tgc gat aga ggt gga gtc gtg atc agc aaa acc ggt Asp Asp Thr Pro Cys Asp Arg Gly Gly Val Val Ile Ser Lys Thr Gly 760	765	770	3198
gag ctg gaa tgc tta ata ggt aag act aca gtg aaa gta ttt agc tgc Glu Leu Glu Cys Leu Ile Gly Lys Thr Thr Val Lys Val Phe Ser Ser 775	780	785	3246
gat aaa aaa ttg gga cct atg cca tgc aga cca aaa gaa gtc ata tcc Asp Lys Lys Leu Gly Pro Met Pro Cys Arg Pro Lys Glu Val Ile Ser 795	800	805	3294
agt gaa gga cgg gtc agc aag ata gct tgc aca ttc aac tac tca aaa Ser Glu Gly Pro Val Ser Lys Ile Ala Cys Thr Phe Asn Tyr Ser Lys 810	815	820	3342
acc ctg gaa aac aaa tac tat gag ccc aga gac agt tat ttc cag caa Thr Leu Glu Asn Lys Tyr Tyr Glu Pro Arg Asp Ser Tyr Phe Gln Gln 825	830	835	3390
tac atg ctc aag gga caa tac caa tac tgg ttc gat ctt gaa gca aca Tyr Met Leu Lys Gly Gln Tyr Gln Tyr Trp Phe Asp Leu Glu Ala Thr 840	845	850	3438
gat cac cac tca gat tac ttt gca gag ttc atc atg ttg gca gtg gta Asp His His Ser Asp Tyr Phe Ala Glu Phe Ile Met Leu Ala Val Val 855	860	865	3486
gcc ctg cta ggg ggg agg tat gtc tta tgg tta atg gtt gtc tac atg Ala Leu Leu Gly Gly Arg Tyr Val Leu Trp Leu Met Val Val Tyr Met 875	880	885	3534
atc ctg gca gat caa atg acc tca gca ata aac ctg ggc caa gga gag Ile Leu Ala Asp Gln Met Thr Ser Ala Ile Asn Leu Gly Gln Gly Glu 890	895	900	3582

gtg gtt ctg ata gga aat tta ata aca cat gag gac cat gag gtg gta Val Val Leu Ile Gly Asn Leu Ile Thr His Glu Asp His Glu Val Val 905 910 915	3630
gta tat ttc ctc ctg tta tac tta ata gtg aag gat gag cca gta aag Val Tyr Phe Leu Leu Leu Tyr Leu Ile Val Lys Asp Glu Pro Val Lys 920 925 930	3678
aag tgg ata ttg ttc ctc ttt cat gct atg acc aac aac cct gta aag Lys Trp Ile Leu Phe Leu Phe His Ala Met Thr Asn Asn Pro Val Lys 935 940 945 950	3726
aca ata tca gtt gga ctg cta atg tta agt ggg cta gtg aag ggg Thr Ile Ser Val Gly Leu Leu Met Leu Ser Gly Leu Val Lys Gly 955 960 965	3771
gaaggggagc gaatgaccta ctgggagggc ctgacctgc agtttacctt gctggtaatg	3831
ataactgcat cactattagt ggcaagaagg gacgttacca catacccttt gataataaca	3891
gtgatagcat taaagaccac ctgggtgaat agtggcccg ggattgatgc agcaatagca	3951
acaatcacga ctgggctatt gatgtggaca tttataagtg actactacaa atacaaacag	4011
tggacgcagt tctgattag tatagtgtct ggtatattcc tcataaggac gctaaaatgg	4071
ataggcgggt tagagttgca cgcacctgaa ttgccatcct acaggccctt attcttcac	4131
ttgacatacc taattctctgc tgcaatagta actagatgga atttagecat agctggcgtg	4191
cttctgcaat gtgtcccccac tatactaatzg gtcttaactt tgtgggcaga tctgttaacg	4251
ctaattctga tactacctac ttatqaacta gccaaactat attacctcaa gggggtgaag	4311
aatggaatgg aaaggaactg gctaggaggg ataacttaca aaagagtgtc agatgtttat	4371
gagatagatg aatcccagga agccgtatat ctgttccct ctaaacagaa ggaagggacg	4431
atcacagggg gtttgcctacc actaataaag gccatactga tcagctgcat tagtagcaag	4491
tggcagtgtc tctacctcct atatctggcg gtggaggtat catactacct ccataagaaa	4551
ataattgaag aagtagcccg gggaaccaat ctaatttcca gactggttgc agccctgttg	4611
gaggtaact ggagatttga caatgaagag accaaggggt taaaaaaatt ctatctgata	4671
tcaggccaag ttaagaatct aataataaaa cataagggtga ggaatgaagt ggtagccac	4731
tggttcaatzg aggaagaggt ctatgggatg cccaagctag tgagtgtagt gaaagcagca	4791
acacttaacc ggagcaggca ttgtatactt tgcacagtct gtgaaagcag agactggaaa	4851
ggagagacct gtccgaagtg tgggagattt gggccttcac tgtcatgtgg gatgacattg	4911
tcagactttg aagagaggca ctataagaa atatttataa gagaagacca atcagacggg	4971
ccttttagag aagagtacaa aggataacct caatacaaa ccaagaggcca gcttttcttg	5031
aggaacctcc cgatattagc tacaanaqta aactattgt tggtagggcaa ttgggatct	5091

gaggtagggg acttggaaac tcttggatgg atcctgagag gtccggcggt gtgcaagaag 5151
ataatagacc atgagaggtg ccatgtatca ataattggaca aattaacagc tttctttggg 5211
atcatgccaa gaggyacgac accaagggcg ccgattagat ttccgacatc tctgtctaaga 5271
atcaggagag gcctcgagac tggatggcg tacacacacc aaggaggaat aagttcagtg 5331
gaccatgtga ctgccggaaa ggacttacta gtatgtgact ccatgggtag aacaagagtc 5391
gtatgccaaa gtaataatag gatgacagat gagactgaat atggagtga aacggactca 5451
ggttggccag aggggtctag gtgctaagtg ttcaaccccg aggcagtga catatcgggg 5511
accaaaggag ccatggtaca tccacagaaa acaggtggtg aatttacttg cgtgacggca 5571
tcaggactc cagctttctt tgacctgaaa aatctgaagg gctggtcagg gctcccaata 5631
tttgaagcal ctagtgggag agtcgtcggg agagttaaaq tagggaagaa tgaggagtca 5691
aagcctacaa aactgatgag tggataacag accggtatcca agagtacaac tgacttaact 5751
gacatggtga aagagataac aacaatgaal agaggggagt ttaagcagat cacactggcc 5811
acgggtgcag gaaagactac agaattacct agggcggtga tagaagaaat aggcccgcc 5871
aaaagagtgt tggctttgat accactcagg gcagcagcag agtcagtata tcaatacatg 5931
aggcagaaac accctagcat agctttccat ctaaggatcg gggaaatga agagggggat 5991
atggccacag gataacata tgctccatat ggctattttt gtcagatgcc tcaacccnaa 6051
ctgagagctg ctatgggtga atacagttac attttccatg atgaatacca ctgtgcaacg 6111
cctgaaccaat tggccataat agyaaaazatt cacaggttt cagaacagtt gcgagtcgtg 6171
gcaatgacgg caacgcccgc tgggaggglg accactacag ggcagaagca cccgatagag 6231
gaatttatag ctccagaagt gatgaagggt gaagalottg gctctgagtt cctggagatt 6291
gcaggcctga aaataccac tgaggaaatg aaaggtaaca tgcctgtatt cgtgccacc 6351
aggaatatgg cagtggagac agcaagaaa ctgaagcca aagggtataa ttctggltac 6411
tactacagtg gaggggccc ggctaacttg agagtagtta catcacagtc gccctatgta 6471
gtagtggcaa ccaatgcaat agagtctgga gtcacattgc cagacctaga tctagttgta 6531
gacaccgggc tgaatgtga gaaaagata cgactgtctt ctaaaatgcc ctccatagtc 6591
accgggttga aaaggtatgc agtgactatt ggggaacagg cacagaaag gggccgggta 6651
gscaggutca agccggggg atactatagg agccaagaga cagcagttgg ctccaaagac 6711
taccactatg atctctaca agcacagaga tatgylatag aggcgggat aaacalaaca 6771
aaatcttca gagagatga ttatgattgg agtctatag aagaagatag cctgatgac 6831
acgcaactag aaatccana taacctattg atatctgag aactaccagt tgcigtgaag 6891
aacaltatgg ccagaacaga ccacctgaa ccaattcaac tggcatacaa cagctatgaa 6951

grccaagtac cagtgtctgtt ccctaagatc aggaatggag aagtaacaga cagctatgac 7011
 agctattcgt tcttgaatgc caggaaactg ggcgacgatg tgccagcata cgtctacgcc 7071
 acggaagatg aagacttggc agtggagcta cttgggtatgg actggcccga cccgggaaac 7131
 caaggtacag ttgaaactgg aagagcatta aaacaagtaa cgggactttc cgctgtctgag 7191
 aacgccttgc tgggtggcttt gtttggatat gtgggggtacc aagccttacc aaaaagacat 7251
 gtgcctatgg tcacggatat atactcaata gaagaccata ggltggaaga cagcacccat 7311
 ctgcagtttg caccacaacc aattagaacg gatggtaaag aaactgagct aaaagaactg 7371
 gcacaaggag acatccagag gtgtgcagag gcaatggttg ggtacgcaca gcaaggggtg 7431
 caattcatca aaacccaagc cctgaagggt caagagaatc atgtattcaa agactcagca 7491
 gacaccatag tggaatacgt agacaagttc atgaaagcaa ttgcagaag taaagatgac 7551
 atcctgaggt atggcctgtg gggggctcac acagctcttt ataaaagcat aggggctagg 7611
 ctaggttatg aaacagcttt tgcaacactg gtgattaaat ggcttgcttt tgggggtgag 7671
 tctataaacg accacgtgaa acaggtgca accgacttag ttgtatatta cataatcaac 7731
 agaccccaat tcccgggaga cactgagaca caacaggagg gccggaaatt cgtggctagc 7791
 tractagtct cagccttggc tacatacacc taaaaagct ggaactatag caatttatca 7851
 aagtggtag agcctgcact tgcttgcttg cctacgctt cccaggcact caaattgctt 7911
 gctccaacgc gcctggagag tgtagtcac ctcagcacag ccattttaca gacttacctg 7971
 gcaatcaggc gtggtaggag tgatggtcta ctgggtacgg gagttagtgc tgccatggag 8031
 atcatgtccc aaaacccgtg atctgttggg atagccgtga tgctgggtgt aggggcogta 8091
 gcggcgcata atgccataga gtcaagttag cagaagagaa cacttttgat gaaggtaatt 8151
 gtgaagaact tcttagatca agcagcaact gatgaactgg tcazagagag cccagagaag 8211
 atcataacgg ctttgtttca ggccgltgca acagtggga accctcttag gttgatatac 8271
 cacttatarg ggtattcta taaaggctgg gaagctaaag aagtagcaga gaaaacagct 8331
 gggcgaact tgttaccct aatcatgttt gaagccgtcg agttgcttgg cgtggacagc 8391
 gagggaaaaga tgaggaggct gtgggtaat tacctgatag agctcctgca gaaactccat 8451
 gacggcttca ggataagcat caaaaagttc gccttaggat gggcaccggg cccattcagc 8511
 tgtaactgga ccccgaggga caataggatc aggcctcccc acgagaacta ccttagagtc 8571
 gtcaccaggt gcagatgtgg gtaccggacg aaggcagtaa aaaactgtgc aggtcagtta 8631
 atactggagg aggaagaggg ctcatcttc tgcagaaaca aatttgggag gggagcacc 8691
 aactacaaag tcacaaaatt ttatgatggc aacctgaag agatcagggc cgtctaaag 8751

ctggagggcc aggttgagat gtattacaaa ggagccacca ttaagattga ttacagcaac 8811
 aataaactta tcctagccac tgataaatgg gaagttgagc acacatacat caccagactc 8871
 acgaaaagat acacaggggc tgggtacaaa ggtgccttcc taggggatga acccaaccac 8931
 aaaagcctga tcgagaggac ctgcgcaacc gtgtgcaagg ataagatata cttttcaaag 8991
 atgaagaaag gctgtgcctt cangtatgat ctatctctaa gcaacttggg aaqattgggc 9051
 gacttgggtc acaggaacaa gcttgaagag aagatatcc cggacgaac tgaacaacg 9111
 tggctggcgt atacattcgt caatgaagac gtgggtacca tcaagccagt cctgggggag 9171
 aaggtcatac cggaaagagag tgatgagata aatttgcaac caacagtaac agtgaatatg 9231
 tctaagtgtc aggtaacagt ggtaggcgag gccaaaaata tgaccacggg ggtggttcca 9291
 ctacagtgta ccaagaggc atgtaatggt caagaccggl cagttctaaa cattggaatg 9351
 gaagaagggg aatacccggt cctgtcgtga agcactgtca ctgtgggtga agctgttcaa 9411
 agtaagatg tgcgccata tgtattgggt atagggtcca ataaggcaac atcaaacagg 9471
 gcaaaagacag ctaagaacgt taagttgtat aaaggaggag atgctgtcga agtcagagac 9531
 ctaaltaaga aaggggagat gctggctgta gcttggccg atgtagaaca ggaacttacta 9591
 gaatatgtag attacaaag cactttctca acaagagaga ccttgggaagc acttagtctg 9651
 ggtaaagcaa aagccaaaaa tataaccaaa gctgatgctc acaggctact caaccagaa 9711
 aaagagcaga ttggattacc tgactgggtc acagctacgg aacctatatt cctggaagct 9771
 atgateaaac aagaaaaata ccacataaca ggggatgtag caaccgtgaa agacaaagcc 9831
 aaacaattag gggccacga ttccacgaga atagttaagg aggtagggtc caggggtgtc 9891
 aacatgaagc ttaatatgctg ggctttgcaa gctgaagag gggatgcaaa cctcaaaccc 9951
 ttatttgaag aactctgct acagtgccta cccgggagaa cagtcaaagg cggaaacctg 10011
 gtgtcgcat accagcttg acaggggaac tggacgcca ctgctgtaa agtatacatg 10071
 gggactataa caqcaaaaag agtaaaaata caccatattg aagcatatat aasattgaag 10131
 gagcttatag aagagtacaa catgaaaagg gtgactggag atccaggtct aagagagacat 10191
 aatgaatgga tcttaagag aatcaaacac caggggaacc tgaggactac gaaataactg 10251
 aaccaggtg aagtagcaga acaactcagc agagaaggtc ataaacaaa tglgtacaac 10311
 aagalaatag gttcaactat ggcatacgtg ggaatcaagc tggagaagct accactagtg 10371
 agggctcaaa cggacacaac ctttttccal caagccatta gggataaaat agacaaagaa 10431
 gagaaccggc agacaccaga cctgcataag gaattgaag aagttttcaa tgccttaaaa 10491
 ataccagaa ctcgtctac ttatgatgca gtggaatgg aggaactgga gacaggtatc 10551
 aacaggaag ggcagctgg ttttttgaa aggaadaaca ttggtgaat actggataca 10611

gagaaaaaca aggtagagga cataattaga gatttaaaat ctggaagacc tatcaagtat 10671
 tacgaaactg caatcccgaa aatgagaag agagatgtca atgatgattg ggagagcggc 10731
 gattttgtag atgaaaagaa accgagagtg atacagtacc cagaggccaa agtcaggcta 10791
 gctataacga aggtcatgta caagtgggtc aaacaaaaac cagtggcat tcccgggtat 10851
 gaaggtaaga caccattgtt tgagatattt gataaggtaa aaaaagaatg gggtagcttc 10911
 gataatccag ttgcagtga ctttgacact aaggcttggg acacacaagt taccagcaaa 10971
 agcctagagc tgattaggga catacagaaa tactatttca agaaggagtg gcataaattc 11031
 attgagacta taactgagca catggtagaa gtgccggtag tcacagctga tggggaggtg 11091
 tacatcagcg agggccaaag aggtagtggc caaccggaca ctagtgtctg caatagtatg 11151
 ttaaatgtct taaccatggc ttatgctttc tgcgagcca caggcgtgcc ctacaaaagt 11211
 ttcaaaaggg ttgccaagat acatgtctgt ggagatgatg gctttttgat aacggagaaa 11271
 agcctaggag aaaaatttgc cagttaagggt atacaaatcc tacatgaagc aggaaaaccc 11331
 cagaaaatta cagaggggga ccgcataaaa gtagcttata agtttgaggc catagaattt 11391
 tgccttcaca cccctgtgcc tgtgaggtgg tcagacaaca ccactagcta tatgccaggt 11451
 aggaacaccg cgactatcct ggctaagatg gccacaaggc tagattcaag tggagaaagg 11511
 gggacaacag catatgagaa ggcagtggct tttagttttc tctgatgta ctcatggac 11571
 cctctgggta gaaggatttg cctacttacg ctatcgagcg agttgggcac caaacctagt 11631
 aaaggacca cctattacta cgaaggcgat ccaatatctg cctataggga ggtgattggc 11691
 cacaacttac tagacctga gaggacaggc ttggagaaac tggcactatt aaacctgagt 11751
 atgtctactc taggtatatg gacaaaacac atcagtaaaa ggttgctaca agactgcgtt 11811
 gatgtaggca gcaaggatgg caattggctg gtaaacgcag ataggccgga gagcagaaaa 11871
 acaggaaagg tctacttgca aagtggaggc cataccgtaa gagggagcca ttatgaagac 11931
 ctgatattgc ctaggatggc gaaacnaaca tttcaaggag tagacagata caaattggga 11991
 cccatagtca acgtaatat cagaaggctg agggttatga tgatggccct ggttggtaga 12051
 gggatgtgaa ccatagctga gcatttcag acaacacgcc aagggccact aaattgtata 12111
 tataactgtg taaatattta cctatttatt tactgttatt tatttaatat agacagtgat 12171
 atttatttaa tagcttatct attattttat ttgatgggat gtagatggca actaactacc 12231
 tcataggacc acactacact catttttaaa actacagcac tttagctgga agggasaagc 12291
 ctgaagtcca gagttggatt aaggaaaaac cctaacagcc cc 12333

40

<211> 100
<212> PRT
<213> Border disease virus

<400> 14

Ser Asp Asp Asn Lys Ser Glu Lys Thr Asn Glu Lys Lys Pro Asp Arg
1 5 10 15

Val Arg Arg Gly Ala Met Lys Ile Thr Pro Lys Glu Ser Glu Lys Asp
20 25 30

Ser Arg Ser Lys Pro Pro Asp Ala Thr Ile Val Val Glu Gly Ile Lys
35 40 45

Tyr Gln Val Lys Lys Lys Gly Lys Val Lys Gly Lys Asn Thr Gln Asp
50 55 60

Gly Leu Tyr His Asn Lys Asn Lys Pro Pro Glu Ser Arg Lys Lys Leu
65 70 75 80

Glu Lys Ala Leu Leu Ala Trp Ala Ile Ile Ala Ile Phe Met Trp Glu
85 90 95

Pro Val Ala Pro
100

<210> 15
<211> 227
<212> PRT
<213> Border disease virus

<400> 15

Glu Asn Val Thr Gln Trp Asn Leu Ser Asp Asn Gly Thr Thr Gly Ile
1 5 10 15

Gln Leu Leu Met Phe Gln Arg Gly Val Asn Arg Ser Leu His Gly Ile
20 25 30

Trp Pro Glu Lys Ile Cys Thr Gly Val Pro Thr His Leu Ala Thr Asp
35 40 45

Ala Glu Leu Lys Gly Ile Gln Gly Met Met Asp Ala Ser Glu Lys Thr
50 55 60

Asn Tyr Thr Cys Cys Arg Leu Gln Arg His Glu Trp Asn Lys Tyr Gly
65 70 75 80

41

Trp Cys Asn Trp Tyr Asn Ile Asn Pro Trp Ile Trp Leu Met Asn Lys
85 90 95

Thr Gln Ala Asn Leu Thr Glu Gly Pro Pro Glu Lys Glu Cys Ala Val
100 105 110

Thr Cys Arg Phe Asp Lys Glu Ala Asp Ile Asn Ile Val Thr Gln Ala
115 120 125

Arg Asp Arg Pro Thr Thr Leu Thr Gly Cys Lys Lys Gly Lys Lys Phe
130 135 140

Ser Phe Ala Gly Met Ile Ile Glu Gly Pro Cys Asn Phe Asn Val Ser
145 150 155 160

Val Glu Asp Ile Leu Phe Gly Asp Asn Glu Cys Ser Ser Leu Phe Gln
165 170 175

Asp Thr Ala Leu Tyr Val Val Asp Gly Val Thr Asn Thr Val Glu Asn
180 185 190

Ala Arg Gln Gly Ala Ala Lys Leu Thr Ser Trp Leu Gly Lys Gln Leu
195 200 205

Gly Ile Met Gly Lys Lys Leu Glu His Lys Ser Lys Thr Trp Phe Gly
210 215 220

Ala Asn Ala
225

<210> 16

<211> 195

<212> PRT

<213> Border disease virus

<400> 16

Gln Ser Pro Tyr Cys Asn Val Thr Arg Lys Ile Gly Tyr Val Trp Tyr
1 5 10 15

Thr Asn Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile Ile
20 25 30

Gly Pro Gly Lys Phe Asp Thr Asn Ala Glu Asp Gly Lys Ile Leu His
35 40 45

Glu Met Arg Gly His Ile Ser Glu Phe Ile Leu Leu Ser Leu Val Val
50 55 60

Ser Arg Gly Phe Phe Arg Phe Arg Gly His Cys Met Ile Gly Pro Arg
50 55 60

43

Tyr Leu Ala Ser Leu His Leu Arg Ala Leu Pro Thr Ser Val Thr Phe
65 70 75 80

Glu Leu Ile Pro Gly Gly Ser Ala Met Thr Glu Glu Glu Met Gly Asp
85 90 95

Asp Phe Glu Phe Gly Leu Cys Pro Cys Asp Ser Arg Pro Val Val Lys
100 105 110

Gly Lys Tyr Asn Thr Thr Leu Leu Asn Gly Ser Ala Phe Gln Leu Ile
115 120 125

Cys Pro Tyr Gly Trp Val Gly Arg Val Glu Cys Thr Thr Val Ser Lys
130 135 140

Ser Thr Leu Ala Thr Glu Val Val Lys Ile Tyr Lys Lys Thr Lys Pro
145 150 155 160

Phe Pro Gln Arg Val Gly Cys Asp His Thr Thr Val Tyr Lys Gln Asp
165 170 175

Leu Tyr His Cys Gln Met Gly Gly Asn Trp Thr Cys Met Arg Gly Glu
180 185 190

Val Val Lys Tyr Val Gly Gly Pro Val Lys Lys Cys Glu Trp Cys Gly
195 200 205

Tyr Val Phe Lys Lys Arg Glu Gly Leu Pro His Tyr Pro Ile Gly Arg
210 215 220

Cys Met Leu Arg Asn Glu Thr Gly Tyr Arg Ser Val Asp Asp Thr Pro
225 230 235 240

Cys Asp Arg Gly Gly Val Val Ile Ser Lys Thr Gly Glu Leu Glu Cys
245 250 255

Ile Ile Gly Lys Thr Thr Val Lys Val Phe Ser Ser Asp Lys Lys Leu
260 265 270

Gly Pro Met Pro Cys Arg Pro Lys Glu Val Ile Ser Ser Glu Gly Pro
275 280 285

Val Ser Lys Ile Ala Cys Thr Phe Asn Tyr Ser Lys Thr Leu Glu Asn
290 295 300

Lys Tyr Tyr Glu Pro Arg Asp Ser Tyr Phe Gln Gln Tyr Met Leu Lys

```
<400> 19
aaaaacaaac ctcaggaatc acgcaagaaa clggaaaaaag cattgttggc gtgggcaata 60
atagctatag ttttgittca agttacaatg ggagaaanaa taacacagtg gaacctataa 120
gataatggga cgcgaaggat acaacgggca atgttcnaaa ggggtgtgaa tagaaqtlla 180
catggaatct ggccagagaa aatctgtact ggcgccctt cccatctagc caccgatata 240
gaactaaaaa caallcargg tatgatggat gcaagtgaga agaccaacta caccgtgttc 300
```

agacttcaac gccatgagtg gaacaagcat gggtgggtgca actggtacaa tattgaaccc 360
 tggattctag tcatgaatag aacccaagcc aatctcactg agggacaacc accaagggag 420
 tgggcagtc cttgtaggta tgatagggct agtgacttaa acgtggtaac acaagctaga 480
 gatagccca cacccttaac aggttgcaag aaaggaaaga actctcctt tgcaggcata 540
 ttgatgctgg gcccttcaa ctttgaaata gctgnaagtg atgtattatt caaagaacat 600
 gaacgcatta gtatgtcca ggataccact ctttacctg ttgacgggtt gaccaactcc 660
 ttagaaggtg ccagacaagg aaccgctaaa ctgacaacct ggttaggcaa gcagctcggg 720
 atactaggaa aaaagtggg aaacagagtg aagacgtggt ttggagcata cgctgcttcc 780
 ccttactgtg atgtcgatcg caaaattggc tacatatggt atacaaaaa ttgcacccct 840
 gcctgcttac ccaagaacac aaaaattgtc ggccctggga aatttggcac caatgcaqag 900
 gacggcaaga tattacatga gatggggggc cactgtcgg aggtactact actttcttta 960
 gtggtgctgt ccgacttcgc accggaaaca gctagttaa gtacctaata cctacatttt 1020
 tccatccac aaagtccgt tgatgtaatg gattgtgata agaccagtt gaacctaca 1080
 gtggagctga caacagctga agtaatacca gggtcggctc ggaatctagg caaatatgta 1140
 tgtataagac caaattggtg gccttatgag acaactgtag tgttggcatt lgaagaggtg 1200
 agccaggtgg tgaagttagt gttgagggca ccagagatt taacacgcat ttggaacgt 1260
 gcaacaacta ctgctttttt agtatgcctt gtaagatag tcaggggcc galgglacag 1320
 ggcattctgt ggctactatt gataacaggg gtacaagggc acttggtattg caaacctga 1380
 ttctcgtatg ccatagcaaa ggacgaaaga attggtcaac tgggggctga aggccttacc 1440
 accactggga aggaatactc acctggaatg aagctggaag acacaatggt cattgcttgg 1500
 tgcgaagatg ggaagttaat gtacctcaa agatgcacga gagaaaccag atatctcgca 1560
 atcttgata caagagcctt gccgaccagt gtggtattca aaaaactctt tgatgggcga 1620
 aagcaagagg atgtagtga aalgaacga acctttgaat ttggaactctg gccatgtgat 1680
 gccaaacca tagtaagagg gaagtrcaat acaacgctgc tgaacggacc ggccttccag 1740
 atggtatgcc ccctaggatg gacagggact gtaagctga cgtcattcaa tatggacacc 1800
 ctagccacaa ctgtggtacg gacatataga aggtctaaac cattccctca taggcaaggc 1860
 tgtatcacc aazagaatct gggggaggat ctccataact gcctccttgg aggaattgg 1920
 attgtgtgc ctggagacca actactatac aaagggggct ctattgaatc ttgcaagtgg 1980
 tgtggctatc aatttaaaga gactgagggg ctaccacaat acccattgg caagtgtaaa 2040
 ttggagaacg agactggtta caggctagta gacagtacct cttgcaatag agaaggtgtc 2100

gccatagtlac cacaagggac attaaagtgc aagataggaa aaacaactgt acaggtcata 2160
 gctatggata ccaaactcgg acctatgect tgcagaccat atgaaatcat atcaagtga 2220
 gggcctgtag aaaagacagc gtgtactttc aactacacta agacattaaa aaataagtat 2280
 tttgagccca gagacagcta ctttcagcaa tacatgctaa aaggagagta tcaatactgg 2340
 tttgacctgg aggtgactga ccatcaccgg gattacttcg ctgagtcocat attagtygtg 2400
 gtagtagccc tcttgggtgg cagatatgta ctttgggtac tggttacata catgggtcta 2460
 tcagaacaga aggccttagg gattcagtat ggatcagggg aagtgggtgat gatgggcaac 2520
 ttgctaaccg ataacaatat tgaagtgglg acalactlcl tgcigtgta cctactgctg 2580
 agggaggaga gcgtaaagaa gtgggtctta ctcttatacc acatcttagt ggtacaccca 2640
 atcaaactcg taattgtgat cctactgatg attggggatg tggtaaaggc ctga 2694

<210> 20
 <211> 900
 <212> PRT
 <213> Bovine viral diarrhea virus : deltaCErnsE1E2p7

<220>
 <221> MISC_FEATURE
 <222> (1)..(34)
 <223> core protein

<220>
 <221> MISC_FEATURE
 <222> (35)..(261)
 <223> Erns

<220>
 <221> MISC_FEATURE
 <222> (262)..(456)
 <223> E1

<220>
 <221> MISC_FEATURE
 <222> (457)..(456)
 <223> E1

<220>
 <221> MISC_FEATURE
 <222> (457)..(830)
 <223> E2

<220>
 <221> MISC_FEATURE
 <222> (831)..(900)
 <223> p7

<400> 20

Met Asn Ser Lys Asn Lys Pro Gln Glu Ser Arg Lys Lys Leu Glu Lys
 1 5 10 15

47

Ala Leu Leu Ala Trp Ala Ile Ile Ala Ile Val Leu Phe Gln Val Thr
20 25 30
Met Gly Glu Asn Ile Thr Gln Trp Asn Leu Gln Asp Asn Gly Thr Glu
35 40 45
Gly Ile Gln Arg Ala Met Phe Gln Arg Gly Val Asn Arg Ser Leu His
50 55 60
Gly Ile Trp Pro Glu Lys Ile Cys Thr Gly Val Pro Ser His Leu Ala
65 70 75 80
Thr Asp Ile Glu Leu Lys Thr Ile His Gly Met Met Asp Ala Ser Glu
85 90 95
Lys Thr Asn Tyr Thr Cys Cys Arg Leu Gln Arg His Glu Trp Asn Lys
100 105 110
His Gly Trp Cys Asn Trp Tyr Asn Ile Glu Pro Trp Ile Leu Val Met
115 120 125
Asn Arg Thr Gln Ala Asn Leu Thr Glu Gly Gln Pro Pro Arg Glu Cys
130 135 140
Ala Val Thr Cys Arg Tyr Asp Arg Ala Ser Asp Leu Asn Val Val Thr
145 150 155 160
Gln Ala Arg Asp Ser Pro Thr Pro Leu Thr Gly Cys Lys Lys Gly Lys
165 170 175
Asn Phe Ser Phe Ala Gly Ile Leu Met Arg Gly Pro Cys Asn Phe Glu
180 185 190
Ile Ala Ala Ser Asp Val Leu Phe Lys Glu His Glu Arg Ile Ser Met
195 200 205
Phe Gln Asp Thr Thr Leu Tyr Leu Val Asp Gly Leu Thr Asn Ser Leu
210 215 220
Glu Gly Ala Arg Gln Gly Thr Ala Lys Leu Thr Thr Trp Leu Gly Lys
225 230 235 240
Gln Leu Gly Ile Leu Gly Lys Lys Leu Glu Asn Lys Ser Lys Thr Trp
245 250 255

Phe Gly Ala Tyr Ala Ala Ser Pro Tyr Cys Asp Val Asp Arg Lys Ile
260 265 270

Gly Tyr Ile Trp Tyr Thr Lys Asn Cys Thr Pro Ala Cys Leu Pro Lys
275 280 285

Asn Thr Lys Ile Val Gly Pro Gly Lys Phe Gly Thr Asn Ala Glu Asp
290 295 300

Gly Lys Ile Leu His Glu Met Gly Gly His Leu Ser Glu Val Leu Leu
305 310 315 320

Leu Ser Leu Val Val Leu Ser Asp Phe Ala Pro Glu Thr Ala Ser Val
325 330 335

Met Tyr Leu Ile Leu His Phe Ser Ile Pro Gln Ser His Val Asp Val
340 345 350

Met Asp Cys Asp Lys Thr Gln Leu Asn Leu Thr Val Glu Leu Thr Thr
355 360 365

Ala Glu Val Ile Pro Gly Ser Val Trp Asn Leu Gly Lys Tyr Val Cys
370 375 380

Ile Arg Pro Asn Trp Trp Pro Tyr Glu Thr Thr Val Val Leu Ala Phe
385 390 395 400

Glu Glu Val Ser Gln Val Val Lys Leu Val Leu Arg Ala Leu Arg Asp
405 410 415

Leu Thr Arg Ile Trp Asn Ala Ala Thr Thr Thr Ala Phe Leu Val Cys
420 425 430

Leu Val Lys Ile Val Arg Gly Gln Met Val Gln Gly Ile Leu Trp Leu
435 440 445

Leu Leu Ile Thr Gly Val Gln Gly His Leu Asp Cys Lys Pro Glu Phe
450 455 460

Ser Tyr Ala Ile Ala Lys Asp Glu Arg Ile Gly Gln Leu Gly Ala Glu
465 470 475 480

Gly Leu Thr Thr Thr Trp Lys Glu Tyr Ser Pro Gly Met Lys Leu Glu
485 490 495

49

Asp Thr Met Val Ile Ala Trp Cys Glu Asp Gly Lys Leu Met Tyr Leu
 500 505 510

Gln Arg Cys Thr Arg Glu Thr Arg Tyr Leu Ala Ile Leu His Thr Arg
 515 520 525

Ala Leu Pro Thr Ser Val Val Phe Lys Lys Leu Phe Asp Gly Arg Lys
 530 535 540

Gln Glu Asp Val Val Glu Met Asn Asp Asn Phe Glu Phe Gly Leu Cys
 545 550 555 560

Pro Cys Asp Ala Lys Pro Ile Val Arg Gly Lys Phe Asn Thr Thr Leu
 565 570 575

Leu Asn Gly Pro Ala Phe Gln Met Val Cys Pro Ile Gly Trp Thr Gly
 580 585 590

Thr Val Ser Cys Thr Ser Phe Asn Met Asp Thr Leu Ala Thr Thr Val
 595 600 605

Val Arg Thr Tyr Arg Arg Ser Lys Pro Phe Pro His Arg Gln Gly Cys
 610 615 620

Ile Thr Gln Lys Asn Leu Gly Glu Asp Leu His Asn Cys Ile Leu Gly
 625 630 635 640

Gly Asn Trp Thr Cys Val Pro Gly Asp Gln Leu Leu Tyr Lys Gly Gly
 645 650 655

Ser Ile Glu Ser Cys Lys Trp Cys Gly Tyr Gln Phe Lys Glu Ser Glu
 660 665 670

Gly Leu Pro His Tyr Pro Ile Gly Lys Cys Lys Leu Glu Asn Glu Thr
 675 680 685

Gly Tyr Arg Leu Val Asp Ser Thr Ser Cys Asn Arg Glu Gly Val Ala
 690 695 700

Ile Val Pro Gln Gly Thr Leu Lys Cys Lys Ile Gly Lys Thr Thr Val
 705 710 715 720

Gln Val Ile Ala Met Asp Thr Lys Leu Gly Pro Met Pro Cys Arg Pro
 725 730 735

Tyr Glu Ile Ile Ser Ser Glu Gly Pro Val Glu Lys Thr Ala Cys Thr

50

740

745

750

Phe Asn Tyr Thr Lys Thr Leu Lys Asn Lys Tyr Phe Glu Pro Arg Asp
755 760 765

Ser Tyr Phe Gln Gln Tyr Met Leu Lys Gly Glu Tyr Gln Tyr Trp Phe
770 775 780

Asp Leu Glu Val Thr Asp His His Arg Asp Tyr Phe Ala Glu Ser Ile
785 790 795 800

Leu Val Val Val Val Ala Leu Leu Gly Gly Arg Tyr Val Leu Trp Leu
805 810 815

Leu Val Thr Tyr Met Val Leu Ser Glu Gln Lys Ala Leu Gly Ile Gln
820 825 830

Tyr Gly Ser Gly Glu Val Val Met Met Gly Asn Leu Leu Thr His Asn
835 840 845

Asn Ile Glu Val Val Thr Tyr Phe Leu Leu Leu Tyr Leu Leu Leu Arg
850 855 860

Glu Glu Ser Val Lys Lys Trp Val Leu Leu Leu Tyr His Ile Leu Val
865 870 875 880

Val His Pro Ile Lys Ser Val Ile Val Ile Leu Leu Met Ile Gly Asp
885 890 895

Val Val Lys Ala
900

<210> 21

<211> 2484

<212> DNA

<213> Bovine viral diarrhea virus : delraCERNsE1E2

<400> 21

aaaaacaaac ctccaggaac acgcaagaaa ctggaaaaag cattgttggc gtgggcaata 60
atagctatag tttgtttca agttacaatg ggagaaaaca taacacagtg gaacctacaa 120
gataatggga cggagaggat acaacgggca atgttccaaa ggggtgtgaa tagaagttta 180
catggaatct ggccagagaa aatctgtact ggcttccctt cccatctagc caccgatata 240
gaactaaaa caattcatgg tangatggat gcaagtga agacaaacta caagtgttgc 300
agatttcaac gcaatgagtg gaacaagcat ggttgggaga actgttataa tattgacccc 360

tggaattctag tcatgaatatg aacccaagcc aatctcactg agggacaacc accaaggagg	420
tgcgagtcac ctgttaggta tgatagggct agtgacttaa acgtggtaac acaagctaga	480
gatagcccca cacccttaac aggttgcaag aaaggaaaga acttctctt tgcaggcata	540
ttgatgcggg gccctgcaa ctttgaaata gctgcaagtg atgtattatt caaagaacat	600
gaacgcatta gtatgttcca ggataccact ctttaccttg ttgacgggtt gaccaactcc	660
ttagaagggtg ccagacaagg aaccgctaaa ctgacaacct ggtagggcaa gcagctcggg	720
atactaggaa aaaagttyga aaacaagagt aagacgtggt ttggagcata cgtgcttcc	780
ccttactgtg atgtcgatcg caaaattggc tacatatggt atacaaaaa ttgcacctt	840
gctgcttac ccaagaacac aaaaattgtc ggccctggga aatttggcac caatgcagag	900
gacggcaaga tattacatga gatgggggggt cacttgtcgg aggtactact actttcttta	960
gtggtgctgt ccgacttcgc accggaaaca gctagtgtaa tctacctaat cctacatttt	1020
tccatcccac aaagtcacgt tgatgtaatg gattgtgata agaccagtt gaacctcaca	1080
gtggagctga caacagctga agtaatacca gggtcgggtct ggaatclagg caaatatgta	1140
tgtataagac caaattgggt gccctatgag accactgtag tgttggcatt tgaagaggtg	1200
agccaggttg tgaagtlagt gttgagggca ctcagagatt taacacgcat ttggaacgct	1260
gcaacaacta cgtctttttt agtatgcctt gtttagatag tcagggggca gatggtacag	1320
ggcattctgt ggctactatt gataacaggg gtacaagggc acttggattg caaacctgaa	1380
ttctcgtatg ccatagcaaa ggacgaaaga atttggtaac tgggggctga aggccttacc	1440
accacttggg aggaatactc acctggaatg aagctggaag acacaatcgt cattgcttgg	1500
tgcgaagatg ggaagltat gtacctccaa agatgcacga gagaaaccag atatctcgca	1560
atcttgcata caagagcctt gccgaccagt gtggtattca aaaaactctt tcatggggca	1620
aagcaugagg atgtagtcga aatgaacgac aactttgaat ttggactctg cccatgtgal	1680
gcaaaaccca tagtaagagg gaagtccaat acaacgctgc tgaacggacc ggccctccag	1740
atggtatgcc ccataggatg gacagggact gtaagctgta cgtcattcaa tatggacacc	1800
rtagccacca ctgtggtacg gacataraga aggtctaac cattccctca taggcaaggc	1860
tgnatcacc aaagaatct gggggaggat ctccataact gcataccttg aggaactlgy	1920
acttgtgtgc ctggagacca actactatac aaagggggct ctattgaatc llgcaagtgg	1980
tgtggctatc aatttaaaga gagttaggga ctaccacact acccatttg caagtgtaaa	2040
ttggagaacg agactgglla caggctaata gacagtaoct cttcaatag agaaggtgtg	2100
gccatagtac cacaaggga acataagtg aagataggaa aacaaactgt acaggtcata	2160
gctatggata ccaaacclgy acctatgctt tgcagaccal atgaatcat atcaagtgg	2220

gggcctgtag aaaagacagc gtgtactttc aactacacta agacattaa aaataagtat 2280
 tttagaccca gagacagcta ctttcagcaa tacatgctaa aaggagagta tcaatactgg 2340
 tttagacctgg aggtgactga ccataccgg gattacttcg ctgagtcacat attagtggg 2400
 gtagtagccc tcttgggtgg cagatatgta ctttgggtac tggttacata catggtctta 2460
 tcagaacaga aggccttagg gtga 2484

<210> 22
 <211> 827
 <212> PRT
 <213> Bovine viral diarrhea virus : deltaCERNsE122

<400> 22

Lys Asn Lys Pro Gln Glu Ser Arg Lys Lys Leu Glu Lys Ala Leu Leu
 1 5 10 15

Ala Trp Ala Ile Ile Ala Ile Val Leu Phe Gln Val Thr Met Gly Glu
 20 25 30

Asn Ile Thr Gln Trp Asn Leu Gln Asp Asn Gly Thr Glu Gly Ile Gln
 35 40 45

Arg Ala Met Phe Gln Arg Gly Val Asn Arg Ser Leu His Gly Ile Trp
 50 55 60

Pro Glu Lys Ile Cys Thr Gly Val Pro Ser His Leu Ala Thr Asp Ile
 65 70 75 80

Glu Leu Lys Thr Ile His Gly Met Met Asp Ala Ser Glu Lys Thr Asn
 85 90 95

Tyr Thr Cys Cys Arg Leu Gln Arg His Glu Trp Asn Lys His Gly Trp
 100 105 110

Cys Asn Trp Tyr Asn Ile Glu Pro Trp Ile Leu Val Met Asn Arg Thr
 115 120 125

Gln Ala Asn Leu Thr Glu Gly Gln Pro Pro Arg Glu Cys Ala Val Thr
 130 135 140

Cys Arg Tyr Asp Arg Ala Ser Asp Ile Asn Val Val Thr Gln Ala Arg
 145 150 155 160

Asp Ser Pro Thr Pro Leu Thr Gly Cys Lys Lys Gly Lys Asn Phe Ser
 165 170 175

Ile Trp Asn Ala Ala Thr Thr Thr Ala Phe Leu Val Cys Leu Val Lys
420 425 430

Ile Val Arg Gly Gln Met Val Gln Gly Ile Leu Trp Leu Leu Ile
435 440 445

Thr Gly Val Gln Gly His Leu Asp Cys Lys Pro Glu Phe Ser Tyr Ala
450 455 460

Ile Ala Lys Asp Glu Arg Ile Gly Gln Leu Gly Ala Glu Gly Leu Thr
465 470 475 480

Thr Thr Trp Lys Glu Tyr Ser Pro Gly Met Lys Leu Glu Asp Thr Met
485 490 495

Val Ile Ala Trp Cys Glu Asp Gly Lys Leu Met Tyr Leu Gln Arg Cys
500 505 510

Thr Arg Glu Thr Arg Tyr Leu Ala Ile Leu His Thr Arg Ala Leu Pro
515 520 525

Thr Ser Val Val Phe Lys Lys Leu Phe Asp Gly Arg Lys Gln Glu Asp
530 535 540

Val Val Glu Met Asn Asp Asn Phe Glu Phe Gly Leu Cys Pro Cys Asp
545 550 555 560

Ala Lys Pro Ile Val Arg Gly Lys Phe Asn Thr Thr Leu Leu Asn Gly
565 570 575

Pro Ala Phe Gln Met Val Cys Pro Ile Gly Trp Thr Gly Thr Val Ser
580 585 590

Cys Thr Ser Phe Asn Met Asp Thr Leu Ala Thr Thr Val Val Arg Thr
595 600 605

Tyr Arg Arg Ser Lys Pro Phe Pro His Arg Gln Gly Cys Ile Thr Gln
610 615 620

Lys Asn Leu Gly Glu Asp Leu His Asn Cys Ile Leu Gly Gly Asn Trp
625 630 635 640

Thr Cys Val Pro Gly Asp Gln Leu Leu Tyr Lys Gly Gly Ser Ile Glu
645 650 655

55

Ser Cys Lys Trp Cys Gly Tyr Gln Phe Lys Glu Ser Glu Gly Leu Pro
660 665 670

His Tyr Pro Ile Gly Lys Cys Lys Leu Glu Asn Glu Thr Gly Tyr Arg
675 680 685

Leu Val Asp Ser Thr Ser Cys Asn Arg Glu Gly Val Ala Ile Val Pro
690 695 700

Gln Gly Thr Leu Lys Cys Lys Ile Gly Lys Thr Thr Val Gln Val Ile
705 710 715 720

Ala Met Asp Thr Lys Leu Gly Pro Met Pro Cys Arg Pro Tyr Glu Ile
725 730 735

Ile Ser Ser Glu Gly Pro Val Glu Lys Thr Ala Cys Thr Phe Asn Tyr
740 745 750

Thr Lys Thr Leu Lys Asn Lys Tyr Phe Glu Pro Arg Asp Ser Tyr Phe
755 760 765

Gln Gln Tyr Met Leu Lys Gly Glu Tyr Gln Tyr Trp Phe Asp Leu Glu
770 775 780

Val Thr Asp His His Arg Asp Tyr Phe Ala Glu Ser Ile Leu Val Val
785 790 795 800

Val Val Ala Leu Leu Gly Gly Arg Tyr Val Leu Trp Leu Leu Val Thr
805 810 815

Tyr Met Val Leu Ser Glu Gln Lys Ala Leu Gly
820 825

<210> 23

<211> 2013

<212> DNA

<213> Bovine viral diarrhea virus : deltaCE1E2p7

<400> 23

aaaaacaaac ctcaggaatc acgcaagaaa ctggaaag cattgttggc gtgggcaata 60
atagctatag ttttgtttca agtlacaaatg ggagcttccc ctactgtga tgcgatogc 120
aaaattggct acatatggta tacaataaat tgcacccctg cctgcttccc caagaacaca 180
aaaattgtcg gccctgggaa atttggcacc aatgcagagg acggcaagat attacatgag 240
atgggggggtc acttctcgga ggtactacta ctctcttttag tgggtctgtc cgacttcgca 300
ccggaaacag ctagtgtaat glacctaatc ctacattttt ccattccaca aagtcacgtt 360

gatgtaatgg attgtgataa gacccaqttg aacctcacag tggagctgac aacagctgaa 420
gtaataccag ggtaggtctg gaattctaggg aaatatgtat gtataagacc aaattggtgg 480
ccttatgaga caactgtagt gttggcattt gaagaggtga gccaggtggg gaagttagtg 540
ttgagggcac tcagagattt aacacgcatt tggaaagctg caacaactac tgttttttta 600
gtatgccttg ttaagatagt caggggccag atggtacagg gcattctgtg gctactattg 660
ataacagggg tacagggca cttggattgc aaacctgaat tctcgtatgc catagcaaag 720
gaagaaagaa ttggtcaact gggggctgaa ggccctacca ccacttgaa ggaatactca 780
cctggaatga agctggaaga cacaatggc attgcttggg gcgaagatgg gaagttaatz 840
tacctccaaa gatgcacgag agaaaccaga tatctcgaa tcttgcatatc aagagccttg 900
ccgaccagtg tggatttcaa aaaactcctt gatgggcgaa agcaagagga tgtagtcgaa 960
atgaacgaca actttgaatt tggactctgc ccattgtatg ccaaaccat agtaagaggg 1020
aagttcaata caacgtctgt gaaggagccg gccttcaga tggatatgcc catagqatgg 1080
acagggactg taagctgtac gtcattcaat atggacacct tagccacaa tgtggtagcg 1140
acatatagaa ggtctaaacc attcctcat aggcgaaggc gtatcaccca aaagaatctg 1200
ggggaggatc tccataactg catccttggg ggaatttggc cttgtgtgac tggagaccaa 1260
ctactatata aagggggctc taltgaatct tgcaagtggg gtggctatca atttaagag 1320
agtgagggac taccacacta cccattggc aagtgtaaal tggagaagga gactggttac 1380
aggctagtag acagtaacct ttgcaataga gaaggtgtgg ccatagtacc acaagggaca 1440
ttaaagtgca agataggaaa acaactgta caggtcatag ctatggatac caaactcggg 1500
cctatgcctt gcagaccala tgaatcata tcaagtgaag qccctgtaga aaagacagcg 1560
tgtactttca actacactaa gacattaaaa aataagtatt ttgagccag agacagctac 1620
tttcagcaat acatgctaaa aggagagtat caatacggg ttgacctgga ggtgactgac 1680
catcacggg attacttgc tgagtcata ttagtgggtg tagtagccct cttgggtggc 1740
acatatgtac tttggttact ggttcacac atgggtctat cagaacagaa ggccttaggg 1800
attcagtatg gatcagggga agtgggtatg atgggcaact tgotaaacca taacaatatt 1860
gaagtggtya catacttctt gctgctgtac ctactgtga gggaggagag cgtaaagaag 1920
tgggtcttac tcttatacca catctttagt gtacacccaa tcaactcgt aattgtgac 1980
ctactgatga ttggggatgt ggtaaaggcc tga 2013

<210> 24
<211> 670
<212> FRT

57

<213> Bovine viral diarrhea virus : deltaCE1E2p7

<400> 24

Lys Asn Lys Pro Gln Glu Ser Arg Lys Lys Leu Glu Lys Ala Leu Leu
1 5 10 15

Ala Trp Ala Ile Ile Ala Ile Val Leu Phe Gln Val Thr Met Gly Ala
20 25 30

Ser Pro Tyr Cys Asp Val Asp Arg Lys Ile Gly Tyr Ile Trp Tyr Thr
35 40 45

Lys Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile Val Gly
50 55 60

Pro Gly Lys Phe Gly Thr Asn Ala Glu Asp Gly Lys Ile Leu His Glu
65 70 75 80

Met Gly Gly His Leu Ser Glu Val Leu Leu Leu Ser Leu Val Val Leu
85 90 95

Ser Asp Phe Ala Pro Glu Thr Ala Ser Val Met Tyr Leu Ile Leu His
100 105 110

Phe Ser Ile Pro Gln Ser His Val Asp Val Met Asp Cys Asp Lys Thr
115 120 125

Gln Leu Asn Leu Thr Val Glu Leu Thr Thr Ala Glu Val Ile Pro Gly
130 135 140

Ser Val Trp Asn Leu Gly Lys Tyr Val Cys Ile Arg Pro Asn Trp Trp
145 150 155 160

Pro Tyr Glu Thr Thr Val Val Leu Ala Phe Glu Glu Val Ser Gln Val
165 170 175

Val Lys Leu Val Leu Arg Ala Leu Arg Asp Leu Thr Arg Ile Trp Asn
180 185 190

Ala Ala Thr Thr Thr Ala Phe Leu Val Cys Leu Val Lys Ile Val Arg
195 200 205

Gly Gln Met Val Gln Gly Ile Leu Trp Leu Leu Leu Ile Thr Gly Val
210 215 220

Gln Gly His Leu Asp Cys Lys Pro Glu Phe Ser Tyr Ala Ile Ala Lys

58

225 230 235 240
 Asp Glu Arg Ile Gly Gln Leu Gly Ala Glu Gly Leu Thr Thr Thr Trp
 245 250 255

 Lys Glu Tyr Ser Pro Gly Met Lys Leu Glu Asp Thr Met Val Ile Ala
 260 265 270

 Trp-Cys Glu Asp Gly Lys Leu Met Tyr Leu Gln Arg Cys Thr Arg Glu
 275 280 285

 Thr Arg Tyr Leu Ala Ile Leu His Thr Arg Ala Leu Pro Thr Ser Val
 290 295 300

 Val Phe Lys Lys Leu Phe Asp Gly Arg Lys Gln Glu Asp Val Val Glu
 305 310 315 320

 Met Asn Asp Asn Phe Glu Phe Gly Leu Cys Pro Cys Asp Ala Lys Pro
 325 330 335

 Ile Val Arg Gly Lys Phe Asn Thr Thr Leu Leu Asn Gly Pro Ala Phe
 340 345 350

 Gln Met Val Cys Pro Ile Gly Trp Thr Gly Thr Val Ser Cys Thr Ser
 355 360 365

 Phe Asn Met Asp Thr Leu Ala Thr Thr Val Val Arg Thr Tyr Arg Arg
 370 375 380

 Ser Lys Pro Phe Pro His Arg Gln Gly Cys Ile Thr Gln Lys Asn Leu
 385 390 395 400

 Gly Glu Asp Leu His Asn Cys Ile Leu Gly Gly Asn Trp Thr Cys Val
 405 410 415

 Pro Gly Asp Gln Leu Leu Tyr Lys Gly Gly Ser Ile Glu Ser Cys Lys
 420 425 430

 Trp Cys Gly Tyr Gln Phe Lys Glu Ser Glu Gly Leu Pro His Tyr Pro
 435 440 445

 Ile Gly Lys Cys Lys Leu Glu Asn Glu Thr Gly Tyr Arg Leu Val Asp
 450 455 460

 Ser Thr Ser Cys Asn Arg Glu Gly Val Ala Ile Val Pro Gln Gly Thr
 465 470 475 480

59

Leu Lys Cys Lys Ile Gly Lys Thr Thr Val Gln Val Ile Ala Met Asp
485 490 495

Thr Lys Leu Gly Pro Met Pro Cys Arg Pro Tyr Glu Ile Ile Ser Ser
500 505 510

Glu Gly Pro Val Glu Lys Thr Ala Cys Thr Phe Asn Tyr Thr Lys Thr
515 520 525

Leu Lys Asn Lys Tyr Phe Glu Pro Arg Asp Ser Tyr Phe Gln Gln Tyr
530 535 540

Met Leu Lys Gly Glu Tyr Gln Tyr Trp Phe Asp Leu Glu Val Thr Asp
545 550 555 560

His His Arg Asp Tyr Phe Ala Glu Ser Ile Leu Val Val Val Val Ala
565 570 575

Leu Leu Gly Gly Arg Tyr Val Leu Trp Leu Leu Val Thr Tyr Met Val
580 585 590

Leu Ser Glu Gln Lys Ala Leu Gly Ile Gln Tyr Gly Ser Gly Glu Val
595 600 605

Val Met Met Gly Asn Leu Leu Thr His Asn Asn Ile Glu Val Val Thr
610 615 620

Tyr Phe Leu Leu Leu Tyr Leu Leu Leu Arg Glu Glu Ser Val Lys Lys
625 630 635 640

Trp Val Leu Leu Leu Tyr His Ile Leu Val Val His Pro Ile Lys Ser
645 650 655

Val Ile Val Ile Leu Leu Met Ile Gly Asp Val Val Lys Ala
660 665 670

<210> 25
<211> 1803
<212> DNA
<213> Bovine viral diarrhea virus : deltaCE1E2

<400> 25
aaaaacaaac ctcaggaatc acgcaagaaa ctggaaaaag cattgttggc gtgggcaata 60
atagctatag ttttgttca agttacaatg ggagcttccc cttactgtga tgctgatcgc 120
aaaattggct acatatggta tacaaaaaat tgcacccctg cctgcttacc caagaacaca 180

aaaattgtcg gccctgggaa atttggcacc aatgcagagg acggcaagat attacatgag 240
 atggggggtc acttgtcgga ggtactacta ctttctttag tgggtgtgtc cgacttcgca 300
 ccggaaacag ctagtgtaat gtacctaate ctacattttt ccatcccaca aagtcacgtt 360
 gatgtaatgg attgtgataa gaccagttg aacctcacag tggagctgac aacagctgaa 420
 gtaataccag ggtcgggtctg gaattctaggc aaatatgtat gtataagacc aaattgggtg 480
 ccttatgaga caactgtagt gttggcattt gaagaggtga gccaggtggt gaagttagtg 540
 ttgagggcac tcagagattt aacacgcatt tggaaacgtg caacaactac tgcttttttā 600
 gtatgccttg ttaagatagt caggggccag atggtacagg gcattctgtg gctactattg 660
 ataacagggg tacaagggca cttggattgc aaacctgaat tctcgtatgc catagcaaag 720
 gacgaaagaa ttggtcaact gggggctgaa ggccttacca ccacttgga ggaatactca 780
 cctggaatga agctggaaga cacaatggc attgcttggg gcgaagatgg gaagttaatg 840
 tacctccaaa gatgcacgag agaaaccaga tatctcgaa tcttgcatatc aagagccttg 900
 ccgaccagtg tggatttcaa aaaactcttt gatgggcgaa agcaagagga tgtagtcgaa 960
 atgaacgaca actttgaatt tggactctgc ccatgtgatg ccaaaccat agtaagaggg 1020
 aagttcaata caacgtgct gaacggaccg gccttcaga tggatatgcc cataggatgg 1080
 acagggactg taagctgtac gtcattcaat atggacacct tagccacaac tgtggtacgg 1140
 acatatagaa ggtctaaacc attccctcat aggcaggct gtatcaccca aaagaatctg 1200
 ggggaggatc tccataactg catccttga ggaaattgga cttgtgtgcc tggagaccaa 1260
 ctactatata aagggggctc tattgaatct tgcaagtggg gtggctatca atttaagag 1320
 agtgagggac taccacta cccattggc aagtgtaaat tggagaacga gactggttac 1380
 aggctagtag acagtacctc tgcgaataga gaaggtgtgg ccatagtacc acaagggaca 1440
 ttaaagtga agataggaaa aacaactgta caggtcatag ctatggatac caaactcgga 1500
 cctatgcctt gcagaccata tgaaatcata tcaagtgagg ggcctgtaga aaagacagcg 1560
 tgtactttca actacactaa gacattaaaa aataagtatt ttgagcccag agacagctac 1620
 tttcagcaat acatgctaaa aggagagtat caatactggg ttgacctgga ggtgactgac 1680
 catcacggg attacttcgc tgagtccata ttagtggtgg tagtagccct cttgggtggc 1740
 agatatgtac tttggttact ggttacatc atggtcttat cagaacagaa ggccttaggg 1800
 tga 1803

<210> 26
 <211> 600
 <212> PRT

<213> Bovine viral diarrhea virus : deltaCE1E2

<400> 26

Lys Asn Lys Pro Gln Glu Ser Arg Lys Lys Leu Glu Lys Ala Leu Leu
1 5 10 15

Ala Trp Ala Ile Ile Ala Ile Val Leu Phe Gln Val Thr Met Gly Ala
20 25 30

Ser Pro Tyr Cys Asp Val Asp Arg Lys Ile Gly Tyr Ile Trp Tyr Thr
35 40 45

Lys Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile Val Gly
50 55 60

Pro Gly Lys Phe Gly Thr Asn Ala Glu Asp Gly Lys Ile Leu His Glu
65 70 75 80

Met Gly Gly His Leu Ser Glu Val Leu Leu Leu Ser Leu Val Val Leu
85 90 95

Ser Asp Phe Ala Pro Glu Thr Ala Ser Val Met Tyr Leu Ile Leu His
100 105 110

Phe Ser Ile Pro Gln Ser His Val Asp Val Met Asp Cys Asp Lys Thr
115 120 125

Gln Leu Asn Leu Thr Val Glu Leu Thr Thr Ala Glu Val Ile Pro Gly
130 135 140

Ser Val Trp Asn Leu Gly Lys Tyr Val Cys Ile Arg Pro Asn Trp Trp
145 150 155 160

Pro Tyr Glu Thr Thr Val Val Leu Ala Phe Glu Glu Val Ser Gln Val
165 170 175

Val Lys Leu Val Leu Arg Ala Leu Arg Asp Leu Thr Arg Ile Trp Asn
180 185 190

Ala Ala Thr Thr Thr Ala Phe Leu Val Cys Leu Val Lys Ile Val Arg
195 200 205

Gly Gln Met Val Gln Gly Ile Leu Trp Leu Leu Leu Ile Thr Gly Val
210 215 220

Gln Gly His Leu Asp Cys Lys Pro Glu Phe Ser Tyr Ala Ile Ala Lys

62

225	230	235	240
Asp Glu Arg Ile Gly Gln Leu Gly Ala Glu Gly Leu Thr Thr Thr Trp	245	250	255
Lys Glu Tyr Ser Pro Gly Met Lys Leu Glu Asp Thr Met Val Ile Ala	260	265	270
Trp Cys Glu Asp Gly Lys Leu Met Tyr Leu Gln Arg Cys Thr Arg Glu	275	280	285
Thr Arg Tyr Leu Ala Ile Leu His Thr Arg Ala Leu Pro Thr Ser Val	290	295	300
Val Phe Lys Lys Leu Phe Asp Gly Arg Lys Gln Glu Asp Val Val Glu	305	310	315
Met Asn Asp Asn Phe Glu Phe Gly Leu Cys Pro Cys Asp Ala Lys Pro	325	330	335
Ile Val Arg Gly Lys Phe Asn Thr Thr Leu Leu Asn Gly Pro Ala Phe	340	345	350
Gln Met Val Cys Pro Ile Gly Trp Thr Gly Thr Val Ser Cys Thr Ser	355	360	365
Phe Asn Met Asp Thr Leu Ala Thr Thr Val Val Arg Thr Tyr Arg Arg	370	375	380
Ser Lys Pro Phe Pro His Arg Gln Gly Cys Ile Thr Gln Lys Asn Leu	385	390	395
Gly Glu Asp Leu His Asn Cys Ile Leu Gly Gly Asn Trp Thr Cys Val	405	410	415
Pro Gly Asp Gln Leu Leu Tyr Lys Gly Gly Ser Ile Glu Ser Cys Lys	420	425	430
Trp Cys Gly Tyr Gln Phe Lys Glu Ser Glu Gly Leu Pro His Tyr Pro	435	440	445
Ile Gly Lys Cys Lys Leu Glu Asn Glu Thr Gly Tyr Arg Leu Val Asp	450	455	460
Ser Thr Ser Cys Asn Arg Glu Gly Val Ala Ile Val Pro Gln Gly Thr	465	470	475
			480

Leu Lys Cys Lys Ile Gly Lys Thr Thr Val Gln Val Ile Ala Met Asp
 485 490 495

Thr Lys Leu Gly Pro Met Pro Cys Arg Pro Tyr Glu Ile Ile Ser Ser
 500 505 510

Glu Gly Pro Val Glu Lys Thr Ala Cys Thr Phe Asn Tyr Thr Lys Thr
 515 520 525

Leu Lys Asn Lys Tyr Phe Glu Pro Arg Asp Ser Tyr Phe Gln Gln Tyr
 530 535 540

Met Leu Lys Gly Glu Tyr Gln Tyr Trp Phe Asp Leu Glu Val Thr Asp
 545 550 555 560

His His Arg Asp Tyr Phe Ala Glu Ser Ile Leu Val Val Val Val Ala
 565 570 575

Leu Leu Gly Gly Arg Tyr Val Leu Trp Leu Leu Val Thr Tyr Met Val
 580 585 590

Leu Ser Glu Gln Lys Ala Leu Gly
 595 600